

GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: March 22, 2006, 12:00:11 ; Search time 68.821 Seconds  
(without alignments)  
2392.073 Million cell updates/sec

Title: US-10-612-668-17  
Perfect score: 2084  
Sequence: 1 MQFGRLVNTFSGVTNLFNSN.....EVDTPNDFGTPTFLASKIG 394

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications\_AA\_Main:  
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2: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep:\*  
3: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep:\*  
4: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep:\*  
5: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep:\*  
6: /cgn2\_6/ptodata/1/pubpaa/US11\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2084	100.0	394	3	US-09-327-180-17
2	2084	100.0	394	5	US-10-612-668-17
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4	2084	100.0	687	5	US-10-612-668-21
5	2084	100.0	688	3	US-09-327-180-23
6	2084	100.0	688	5	US-10-612-668-23
7	1837	88.1	752	3	US-09-327-180-2
8	1837	88.1	752	5	US-10-612-668-2
9	1234.5	59.2	667	4	US-10-108-260A-3778
10	494.5	23.7	877	6	US-11-097-143-14664
11	324	15.5	1330	4	US-10-108-260A-3237
12	313.5	15.0	1549	6	US-11-097-143-1776
13	313.5	15.0	1549	6	US-11-097-143-29028
14	302.5	14.5	2443	6	US-11-097-143-8355
15	301	14.4	786	4	US-10-164-080-2
16	301	14.4	786	4	US-10-299-327-2
17	301	14.4	786	4	US-10-128-174-13
18	301	14.4	786	4	US-10-128-174-31
19	301	14.4	786	4	US-10-128-174-32
20	301	14.4	786	4	US-10-128-174-33
21	301	14.4	787	3	US-09-866-050A-334
22	300.5	14.4	347	4	US-10-128-174-30
23	300.5	14.4	1724	3	US-09-364-899-43
24	300.5	14.4	1724	5	US-10-975-523-43
25	296	14.2	1094	5	US-10-479-764-22
26	296	14.2	1097	5	US-10-450-763-52300
27	296	14.2	3913	4	US-10-334-143-45

28	296	14.2	4274	5	US-10-450-763-31331	Sequence 31331, A
29	296	14.2	4377	5	US-10-756-149-4917	Sequence 4917, Ap
30	296	14.2	4386	5	US-10-450-763-37734	Sequence 37734, A
31	296	14.2	4397	5	US-10-450-763-52303	Sequence 52303, A
32	288	13.8	1762	4	US-10-205-194-117	Sequence 117, App
33	283.5	13.6	784	4	US-10-164-080-7	Sequence 7, Appli
34	283.5	13.6	784	4	US-10-258-951-70	Sequence 70, Appl
35	283.5	13.6	784	5	US-10-923-035-56	Sequence 56, Appl
36	283.5	13.6	784	5	US-10-990-000-70	Sequence 70, Appl
37	283.5	13.5	784	4	US-10-354-358-38	Sequence 38, Appl
38	281.5	13.5	784	4	US-10-128-174-12	Sequence 12, Appl
39	281.5	13.5	784	4	US-10-658-904-2	Sequence 2, Appli
40	281.5	13.5	720	4	US-10-433-794-20	Sequence 20, Appl
41	280.5	13.5	765	4	US-10-128-174-3	Sequence 3, Appli
42	280.5	13.5	765	4	US-10-128-174-34	Sequence 34, Appl
43	280.5	13.5	765	4	US-10-128-174-35	Sequence 35, Appl
44	280.5	13.5	765	4	US-10-128-174-36	Sequence 36, Appl
45	280.5	13.5	765	4	US-10-128-174-37	Sequence 37, Appl

ALIGNMENTS

RESULT 1

US-09-927-180-17  
; Sequence 17, Application US/09927180  
; Patent No. US2002010634A1  
; GENERAL INFORMATION:  
; APPLICANT: Jones, Simon  
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B  
; NUMBER OF SEQUENCES: 25  
; CORRESPONDENCE ADDRESS:  
; ADDRESSER: Genetics Institute, Inc.  
; STREET: 87 Cambridgepark Drive  
; CITY: Cambridge  
; STATE: Massachusetts  
; COUNTRY: U.S.A.  
; ZIP: 02140  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25 (BPO)  
; CURRENT APPLICATION NUMBER: US/09/927,180  
; FILING DATE: 09-Aug-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/519,223  
; FILING DATE: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Brown, Scott A.  
; REGISTRATION NUMBER: 32,724  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 498-8224  
; TELEFAX: (617) 876-5851  
; INFORMATION FOR SEQ ID NO: 17:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 394 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 17:  
US-09-927-180-17

Query Match 100.0%; Score 2084; DB 3; Length 394;  
Best Local Similarity 100.0%; Pred. No. 6.5e-191;  
Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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DB 1 MQFGRLVNTFSGVTNLFNSNPRVKEVAVADYSSDRVREGQLILFQNTPNRTWDCVILV 60

QY 61 NPRNSQSGFRLQLEADALVNFHOYSSQLLPFYESSQVLHTEVLOHLDLIRNHPW 120  
DB 61 NPRNSQSGFRLQLEADALVNFHOYSSQLLPFYESSQVLHTEVLOHLDLIRNHPW 120  
QY 121 SVAHLAVELGIRECFHHSRIISCANCAENEBGCTPLHLACRKGDEILVELVOYCHTQMD 180  
DB 121 SVAHLAVELGIRECFHHSRIISCANCAENEBGCTPLHLACRKGDEILVELVOYCHTQMD 180  
QY 181 VTDYGETVFHYAVQDQNSQVLQLGRNAVAGLNVNNOGLTPLHLACOLGQKQEMVRVLL 240  
DB 181 VTDYGETVFHYAVQDQNSQVLQLGRNAVAGLNVNNOGLTPLHLACOLGQKQEMVRVLL 240  
QY 241 LCNARCINMGNGYPPIHSAMKFSQKCAEMIISMDSQIHSKDPYRGASPLHWAKNAEMA 300  
DB 241 LCNARCINMGNGYPPIHSAMKFSQKCAEMIISMDSQIHSKDPYRGASPLHWAKNAEMA 300  
QY 301 RMLLKRGCVNSTSSAGNTALHVGVMNRFDCAIVLLTHGANADARGHGNTPLHLAMSK 360  
DB 301 RMLLKRGCVNSTSSAGNTALHVGVMNRFDCAIVLLTHGANADARGHGNTPLHLAMSK 360  
QY 361 DNVEMIKALIVFGAEVDTNDFGETPTFLASKIG 394  
DB 361 DNVEMIKALIVFGAEVDTNDFGETPTFLASKIG 394

RESULT 2  
US-10-612-668-17  
; Sequence 17, Application US/10612668  
; Publication No. US20050196852A1  
; GENERAL INFORMATION:  
; APPLICANT: Jones, Simon  
; Tang, Jim  
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B  
; NUMBER OF SEQUENCES: 25  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genetics Institute, Inc.  
; STREET: 87 CambridgePark Drive  
; CITY: Cambridge  
; STATE: Massachusetts  
; COUNTRY: U.S.A.  
; ZIP: 02140  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/612,668  
; FILING DATE: 01-Jul-2003  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/09/927,180  
; FILING DATE: 09-Aug-2001  
; APPLICATION NUMBER: 09/519,223  
; FILING DATE: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Brown, Scott A.  
; REGISTRATION NUMBER: 32,724  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 498-8224  
; TELEFAX: (617) 876-5851  
; INFORMATION FOR SEQ ID NO: 17:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 394 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 17:  
US-10-612-668-17  
Query Match 100.0%; Score 2084; DB 5; Length 394;  
Best Local Similarity 100.0%; Pred. No. 6.5e-191;

Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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DB 1 MOFFRLVNTSGVTNLFNSNPRVKEVAVADYTSDDRVREEQQLILFQNTNRTWDCVILV 60  
QY 61 NPRNSQSGFRLQLEADALVNFHOYSSQLLPFYESSQVLHTEVLOHLDLIRNHPW 120  
DB 61 NPRNSQSGFRLQLEADALVNFHOYSSQLLPFYESSQVLHTEVLOHLDLIRNHPW 120  
QY 121 SVAHLAVELGIRECFHHSRIISCANCAENEBGCTPLHLACRKGDEILVELVOYCHTQMD 180  
DB 121 SVAHLAVELGIRECFHHSRIISCANCAENEBGCTPLHLACRKGDEILVELVOYCHTQMD 180  
QY 181 VTDYGETVFHYAVQDQNSQVLQLGRNAVAGLNVNNOGLTPLHLACOLGQKQEMVRVLL 240  
DB 181 VTDYGETVFHYAVQDQNSQVLQLGRNAVAGLNVNNOGLTPLHLACOLGQKQEMVRVLL 240  
QY 241 LCNARCINMGNGYPPIHSAMKFSQKCAEMIISMDSQIHSKDPYRGASPLHWAKNAEMA 300  
DB 241 LCNARCINMGNGYPPIHSAMKFSQKCAEMIISMDSQIHSKDPYRGASPLHWAKNAEMA 300  
QY 301 RMLLKRGCVNSTSSAGNTALHVGVMNRFDCAIVLLTHGANADARGHGNTPLHLAMSK 360  
DB 301 RMLLKRGCVNSTSSAGNTALHVGVMNRFDCAIVLLTHGANADARGHGNTPLHLAMSK 360  
QY 361 DNVEMIKALIVFGAEVDTNDFGETPTFLASKIG 394  
DB 361 DNVEMIKALIVFGAEVDTNDFGETPTFLASKIG 394  
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US-09-927-180-21  
; Sequence 21, Application US/09927180  
; Patent No. US20020106364A1  
; GENERAL INFORMATION:  
; APPLICANT: Jones, Simon  
; Tang, Jim  
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B  
; NUMBER OF SEQUENCES: 25  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genetics Institute, Inc.  
; STREET: 87 CambridgePark Drive  
; CITY: Cambridge  
; STATE: Massachusetts  
; COUNTRY: U.S.A.  
; ZIP: 02140  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/927,180  
; FILING DATE: 09-Aug-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/519,223  
; FILING DATE: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Brown, Scott A.  
; REGISTRATION NUMBER: 32,724  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 498-8224  
; TELEFAX: (617) 876-5851  
; INFORMATION FOR SEQ ID NO: 21:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 687 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 21:  
US-09-927-180-21

GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: March 22, 2006, 12:01:45 ; Search time 8.60262 Seconds  
(without alignments)  
1310.928 Million cell updates/sec

Title: US-10-612-668-17  
Perfect score: 2084  
Sequence: 1 MQPFGRLVNTFSGVTNLFNS.....EVDTPNDGFTPTFLASKIG 394

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 169630 seqs, 28622889 residues

Total number of hits satisfying chosen parameters: 169630

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications\_AA\_New:  
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2: /cgn2\_6/ptodata/1/pubppaa/US06\_NEW\_PUB.pap:  
3: /cgn2\_6/ptodata/1/pubppaa/US07\_NEW\_PUB.pap:  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	310	14.9	1159	6	US-10-055-877-139
2	296	14.2	4384	6	US-10-821-234-1120
3	293	14.1	1765	6	US-10-055-877-140
4	293	14.1	1940	6	US-10-055-877-141
5	278.5	13.4	784	7	US-11-072-175-153
6	271.5	13.0	1059	6	US-10-055-877-138
7	249	11.9	791	6	US-10-055-877-137
8	244	11.7	237	7	US-11-096-568A-28113
9	244	11.7	247	7	US-11-096-568A-28112
10	234	11.2	1431	6	US-10-501-035-220
11	231	11.1	795	7	US-11-072-512-2378
12	230	11.0	993	6	US-10-055-877-6
13	229.5	11.0	240	7	US-11-096-568A-22417
14	229.5	11.0	244	7	US-11-096-568A-22416
15	227.5	10.9	645	7	US-11-072-512-2588
16	223	10.7	219	7	US-11-096-568A-28114
17	219.5	10.5	505	7	US-11-072-512-2553
18	213	10.2	241	7	US-11-096-568A-9945
19	213	10.2	245	7	US-11-096-568A-9944
20	213	10.2	280	7	US-11-096-568A-9943
21	206.5	9.9	657	7	US-11-072-512-2529
22	204	9.8	835	7	US-11-186-283-8
23	202	9.7	2471	7	US-11-050-346-68
24	200	9.6	656	7	US-11-234-786-379
25	200	9.6	671	7	US-11-234-786-380

Sequence 378, App  
Sequence 67, Appl  
Sequence 376, App  
Sequence 2, Appl  
Sequence 532, App  
Sequence 16312, A  
Sequence 16312, A  
Sequence 11369, A  
Sequence 11368, A  
Sequence 11367, A  
Sequence 975, App  
Sequence 10314, A  
Sequence 10313, A  
Sequence 219, App  
Sequence 2283, App  
Sequence 3095, App  
Sequence 377, App  
Sequence 12768, A  
Sequence 12767, A

## ALIGNMENTS

RESULT 1  
US-10-055-877-139  
; Sequence 139, Application US/10055877  
; Publication No. US2005028241A1  
; GENERAL INFORMATION:

; APPLICANT: DeCristofaro, Marc  
; APPLICANT: Padigaru, Muralidhara  
; APPLICANT: Miller, Charles  
; APPLICANT: Tchernev, Vellizar  
; APPLICANT: Zhong, Mei  
; APPLICANT: Anderson, David  
; APPLICANT: Ballinger, Robert  
; APPLICANT: Gerlach, Valerie  
; APPLICANT: Spytek, Kimberly  
; APPLICANT: Ratelli, Luca  
; APPLICANT: Kekuda, Ramesh  
; APPLICANT: Guo, Xiaojia  
; APPLICANT: Zerhusen, Bryan  
; APPLICANT: Andrew, David  
; APPLICANT: Mezes, Peter  
; APPLICANT: Patturajan, Meera  
; APPLICANT: Burgess, Catherine  
; APPLICANT: Eisen, Andrew  
; APPLICANT: Wolenc, Adam  
; APPLICANT: Baumgartner, Jason  
; APPLICANT: Shinkets, Richard  
; APPLICANT: Gusev, Vladimir  
; APPLICANT: Vernet, Corine  
; APPLICANT: Taupier Jr., Raymond  
; APPLICANT: Pena, Carol  
; APPLICANT: Shenoy, Suresh  
; APPLICANT: Li, Li  
; APPLICANT: Casman, Stacie  
; APPLICANT: Boldog, Ference  
; TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoded Thereby  
; FILE REFERENCE: 21402-251  
; CURRENT APPLICATION NUMBER: US/10/055,877  
; PRIOR FILING DATE: 2002-01-22  
; PRIOR APPLICATION NUMBER: 60/262,892  
; PRIOR FILING DATE: 2001-01-19  
; PRIOR APPLICATION NUMBER: 60/263,598  
; PRIOR FILING DATE: 2001-01-23  
; PRIOR APPLICATION NUMBER: 60/263,799  
; PRIOR FILING DATE: 2001-01-24  
; PRIOR APPLICATION NUMBER: 60/264,117  
; PRIOR FILING DATE: 2001-01-25  
; PRIOR APPLICATION NUMBER: 60/264,139  
; PRIOR FILING DATE: 2001-01-25

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; PRIOR APPLICATION NUMBER: 60/264,478
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/263,351
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 60/272,870
; PRIOR FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: 60/275,990
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/275,927
; PRIOR FILING DATE: 2001-03-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 512
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 139
; LENGTH: 1159
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-10-055-877-139

Query Match      14.9%; Score 310; DB 6; Length 1159;
Best Local Similarity 27.8%; Pred. No. 1.7e-21;
Matches 95; Conservative 64; Mismatches 117; Indels 66; Gaps 11;

QY 103 MTEVLQHTDLIRNPS-----MSVAHLA-----VELGIRECFHSHRSIIISCANCA 147
DB 349 HVRVAKLLD--RNADANARALNGFTPLHIACKNRLKVVELLR---HGASIS----A 398
QY 148 ENEECTPLHLACRGDGEILLVELVQYCHTQMDVTDYKGTVFHYVAVQGDNSQVQLLGR 207
DB 399 TTESGLTPLHVAFAFGCMNVIVYLQH--DASPDVPTVRGETPLHIAARANOTDIIRILLR 457
QY 208 NAVAGLNQVNNGLTPLHLACQLGKQEMVRVLLLCNARC----- 247
DB 458 NG-AQVDARAREQQTPLHIAASLGNVDIVMLLQHGQVDATTKDMYTALHIAAKEGODE 516
QY 248 ---IMPNG-----YPIHSAKPSQKCAEMIISMDSSQIHSKDPRIYASPLHW 293
DB 517 VAAVLIENGALDAATKKGFTPLHLTKYGHKVAQLLQKEADV--DAQGKNGVTPLHV 574
QY 294 A---KNAEWARMLLKRCNVNSTSAGNTALHVGVMRNFDCAI VLLTHGANADARGEHG 350
DB 575 ACHYNNQVALLLEKSGASPHATKNGHTPLHIAARKNQMDTATTLLEYGALANAESKAG 634
QY 351 NPLHLAMSKNVEMIKALIVFGAEVDPDNDFTPTFLASK 392
DB 635 FTPLHLSQEGHAEISNLLIEHKAAVNHPAKNGLTPMLHCAQ 676

RESULT 2
US-10-821-234-1120
; Sequence 1120, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Ton
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt seq_genes Version 1.0
; SEQ ID NO 1120
; LENGTH: 4384
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1120

Query Match      14.2%; Score 296; DB 6; Length 4384;
Best Local Similarity 29.2%; Pred. No. 2.6e-19;
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Matches 81; Conservative 54; Mismatches 130; Indels 12; Gaps 6;
QY 124 HLAVELGIRECFHSHRSIIISCANCAENEBCCTPLHLACKGDEILLVELVQYCHTQMDVTD 183
DB 511 HISARLGKADIVQQLLOQGASPNATTSYTPHLHSAREGHEDVNAFLD--GASLSITT 569
QY 184 YKGETVFHYAVQGDNSQVQLLGRNAVAGLNQVNNGLTPLHLACQLGKQEMVRVLLCN 243
DB 570 KKGFTPLHVAAYKGLKLEVANLLQKS--ASPDAGKSGLTPLHVAAHYDNQKVALLLDOG 628
QY 244 ARCNIMNGY-PIHSAMKFSQKCAEMI--SWDSSQIHSKDPRIYASPLHW---NA 297
DB 629 ASPHAAAKNGYTPHLHIAAKNQMDIATTLLEYGADANAV---TQGIASVHLAAQEGHV 684
QY 298 EMARMLLKRCNVNSTSAGNTALHVGVMRNFDCAI VLLTHGANADARGEHNTPLHLA 357
DB 685 DMVSLLLGRNAVNLNKSGLTPLHLAAQEDRVNVAEVLVNNQGAHVDAQTCKGYTPLHVG 744
QY 358 MSKDNVEMIKALIVFGAEVDPDNDFTPTFLASKIG 394
DB 745 CHYGNIKIVNPLQLHSAKVNKTKNGYTPHLHQAQOG 781

RESULT 3
US-10-055-877-140
; Sequence 140, Application US/10055877
; Publication No. US20050289241A1
; GENERAL INFORMATION:
; APPLICANT: DeCristofaro, Marc
; APPLICANT: Padigar, Murallidhara
; APPLICANT: Miller, Charles
; APPLICANT: Tchernev, Velizar
; APPLICANT: Zhong, Mei
; APPLICANT: Anderson, David
; APPLICANT: Ballinger, Robert
; APPLICANT: Gerlach, Valerie
; APPLICANT: Spytek, Kimberly
; APPLICANT: Ratelli, Luca
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Guo, Xiaojia
; APPLICANT: Zehusen, Bryan
; APPLICANT: Andrew, David
; APPLICANT: Mezes, Peter
; APPLICANT: Patturajan, Meera
; APPLICANT: Burgess, Catherine
; APPLICANT: Eisen, Andrew
; APPLICANT: Wolenc, Adam
; APPLICANT: Baumgartner, Jason
; APPLICANT: Shimkets, Richard
; APPLICANT: Gusev, Vladimir
; APPLICANT: Vernet, Corine
; APPLICANT: Taupier Jr., Raymond
; APPLICANT: Pena, Carol
; APPLICANT: Shenoy, Suresh
; APPLICANT: Li, Li
; APPLICANT: Casman, Stacie
; APPLICANT: Boldog, Perence
; TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoded Thereby
; FILE REFERENCE: 21402-251
; CURRENT APPLICATION NUMBER: US/10/055,877
; CURRENT FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: 60/262,892
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: 60/263,598
; PRIOR FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: 60/263,799
; PRIOR FILING DATE: 2001-01-24
; PRIOR APPLICATION NUMBER: 60/264,117
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 60/264,139
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 60/264,478
; PRIOR FILING DATE: 2001-01-26
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GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: March 22, 2006, 11:25:51 ; Search time 20.4551 Seconds  
(without alignments)  
1592.473 Million cell updates/sec

Title: US-10-612-668-17  
Perfect score: 2084  
Sequence: 1 MQFFGLVNTSGVTNLFNS.....EVDTPNDFGTFPLASKIG 394

Scoring table: BLOSUM62  
Gapop: 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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3: /cgn2\_6/ptodata/1/iaa/H COMB.pap:\*  
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6: /cgn2\_6/ptodata/1/iaa/backfilea1.pap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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12	1837	88.1	752	1	US-08-422-106-2
13	1837	88.1	752	1	US-08-735-716-2
14	1837	88.1	752	1	US-08-555-568B-2
15	1837	88.1	752	2	US-09-519-223-2
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19	359.5	17.3	545	2	US-09-270-767-61684
20	338	16.2	843	1	US-09-172-977-3
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23	332	15.9	1839	2	US-09-404-108-4
24	332	15.9	2753	2	US-09-519-223-2
25	332	15.9	2753	2	US-09-519-223-2
26	332	15.9	3924	2	US-09-538-092-1246
27	305.5	14.7	1745	1	US-09-031-485-33

28	305.5	14.7	1745	1	US-08-847-429A-33	Sequence 33, Appl
29	305.5	14.7	1745	2	US-09-065-474-33	Sequence 33, Appl
30	305.5	14.7	1745	2	US-09-557-034-33	Sequence 33, Appl
31	301	14.4	786	2	US-09-509-802-2	Sequence 2, Appli
32	301	14.4	787	2	US-09-188-930-334	Sequence 334, App
33	301	14.4	787	2	US-09-312-283C-334	Sequence 334, App
34	300.5	14.4	1724	2	US-09-964-899-43	Sequence 43, Appl
35	296	14.2	1088	2	US-09-082-059-2	Sequence 2, Appli
36	296	14.2	3913	2	US-09-949-016-10933	Sequence 10933, A
37	296	14.2	4377	2	US-09-949-016-6978	Sequence 6978, Ap
38	294	14.1	1719	2	US-09-949-016-6966	Sequence 6966, Ap
39	294	14.1	1856	2	US-09-949-016-5876	Sequence 5876, Ap
40	294	14.1	1880	2	US-09-949-016-5876	Sequence 5876, Ap
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43	294	14.1	1883	2	US-09-949-016-9011	Sequence 9011, Ap
44	294	14.1	1883	2	US-09-949-016-9012	Sequence 9012, Ap
45	294	14.1	1883	2	US-09-949-016-9013	Sequence 9013, Ap

ALIGNMENTS

RESULT 1  
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; Sequence 17, Application US/08555568B  
; Patent No. 5976854  
; GENERAL INFORMATION:  
; APPLICANT: Jones, Simon  
; APPLICANT: Tang, Jim  
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B  
; NUMBER OF SEQUENCES: 25  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genetics Institute, Inc.  
; STREET: 87 CambridgePark Drive  
; CITY: Cambridge  
; STATE: Massachusetts  
; COUNTRY: U.S.A.  
; ZIP: 02140  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/555,568B  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Brown, Scott A.  
; REGISTRATION NUMBER: 32,724  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 498-8224  
; TELEFAX: (617) 876-5851  
; INFORMATION FOR SEQ ID NO: 17:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 394 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-555-568B-17

Query Match	100.0%;	Score 2084;	DB 1;	Length 394;
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DB 241 LCNARCNIMGNGYPIHSAKFSQKCAEMIISMSSQIHSKDPKRYGASPLHWAKNAENA 300  
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DB 301 RMLLKRCGCVNSTSSAGNTALHVGVMNRNFDCAI VLLTHGANADARGEHNTPLHLAMSK 360  
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RESULT 2

US-09-519-223-17  
; Sequence 17, Application US/09519223  
; Patent No. 6274140  
; GENERAL INFORMATION:  
; APPLICANT: Jones, Simon  
; APPLICANT: Tang, Jim  
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B  
; NUMBER OF SEQUENCES: 25  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genetics Institute, Inc.  
; STREET: 87 CambridgePark Drive  
; CITY: Cambridge  
; STATE: Massachusetts  
; COUNTRY: U.S.A.  
; ZIP: 02140  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/519,223  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/555,568  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Brown, Scott A.  
; REGISTRATION NUMBER: 32,724  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 498-8224  
; TELEFAX: (617) 876-5851  
; INFORMATION FOR SEQ ID NO: 17:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 394 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-519-223-17

Query Match 100.0%; Score 2084; DB 2; Length 394;  
Best Local Similarity 100.0%; Pred. No. 2.4e-226;  
Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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DB 241 LCNARCNIMGNGYPIHSAKFSQKCAEMIISMSSQIHSKDPKRYGASPLHWAKNAENA 300  
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DB 301 RMLLKRCGCVNSTSSAGNTALHVGVMNRNFDCAI VLLTHGANADARGEHNTPLHLAMSK 360  
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RESULT 3

US-09-927-180-17  
; Sequence 17, Application US/09927180  
; Patent No. 6645736  
; GENERAL INFORMATION:  
; APPLICANT: Jones, Simon  
; APPLICANT: Tang, Jim  
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B  
; NUMBER OF SEQUENCES: 25  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genetics Institute, Inc.  
; STREET: 87 CambridgePark Drive  
; CITY: Cambridge  
; STATE: Massachusetts  
; COUNTRY: U.S.A.  
; ZIP: 02140  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/927,180  
; FILING DATE: 09-Aug-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/519,223  
; FILING DATE: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Brown, Scott A.  
; REGISTRATION NUMBER: 32,724  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 498-8224  
; TELEFAX: (617) 876-5851  
; INFORMATION FOR SEQ ID NO: 17:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 394 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 17:  
US-09-927-180-17

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Best Local Similarity 100.0%; Pred. No. 2.4e-226;  
Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.  
OM protein - protein search, using sw model  
Run on: March 22, 2006, 12:00:11 ; Search time 51.0044 Seconds  
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Perfect score: 1531  
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Maximum Match 100%  
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- 3: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep:\*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	1531	100.0	688	3	US-09-927-180-23
6	1531	100.0	688	5	US-10-612-668-23
7	1524	99.5	667	4	US-10-108-260A-3778
8	1471	96.1	752	3	US-09-927-180-2
9	1471	96.1	752	5	US-10-612-668-2
10	736	48.1	877	6	US-11-097-143-14664
11	456.5	29.8	1071	4	US-10-369-493-6885
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13	419	27.4	1023	4	US-10-369-493-6690
14	261	17.0	468	4	US-10-369-493-4998
15	245	16.0	1053	4	US-10-425-115-196524
16	235	15.3	1254	4	US-10-437-963-169583
17	234	15.3	387	4	US-10-421-654-66
18	234	15.3	387	5	US-10-796-907-66
19	211.5	13.8	370	3	US-09-925-300-1483
20	211.5	13.8	562	5	US-10-786-505-21
21	211.5	13.8	661	5	US-10-786-505-18
22	211.5	13.8	682	5	US-10-181-069-9
23	211.5	13.8	682	5	US-10-786-505-15
24	211.5	13.8	782	5	US-10-786-505-1
25	208.5	13.6	350	4	US-10-421-654-100
26	208.5	13.6	350	5	US-10-796-907-100
27	207.5	13.6	308	5	US-10-796-907-132

28	204.5	13.4	577	4	US-10-310-154-616	Sequence 616, App
29	201	13.1	315	4	US-10-424-599-259117	Sequence 259117,
30	201	13.1	382	4	US-10-310-154-615	Sequence 615, App
31	195.5	12.8	382	4	US-10-424-599-258423	Sequence 258423,
32	193.5	12.6	387	4	US-10-437-963-177823	Sequence 177823,
33	190	12.4	378	4	US-10-421-654-18	Sequence 18, Appl
34	190	12.4	378	5	US-10-796-907-18	Sequence 18, Appl
35	182	11.9	37	6	US-11-028-376-13	Sequence 13, Appl
36	182	11.9	37	6	US-11-010-558-6	Sequence 6, Appli
37	178	11.6	435	4	US-10-425-115-343159	Sequence 343159,
38	177	11.6	410	3	US-09-755-630A-290	Sequence 290, App
39	177	11.6	410	3	US-09-755-630A-292	Sequence 292, App
40	177	11.6	410	5	US-10-658-180-290	Sequence 290, App
41	177	11.6	410	5	US-10-658-180-292	Sequence 292, App
42	177	11.6	410	5	US-10-682-011-10	Sequence 10, Appl
43	177	11.6	410	5	US-10-682-011-12	Sequence 12, Appl
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45	177	11.6	437	4	US-10-425-114-39376	Sequence 39376, A

ALIGNMENTS

RESULT 1  
US-09-927-180-19  
; Sequence 19, Application US/09927180  
; Patent No. US20020106364A1  
; GENERAL INFORMATION:  
; APPLICANT: Tang, Jim  
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B  
; NUMBER OF SEQUENCES: 25  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: Genetics Institute, Inc.  
; STREET: 87 CambridgePark Drive  
; CITY: Cambridge  
; STATE: Massachusetts  
; COUNTRY: U.S.A.  
; ZIP: 02140  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)  
; CURRENT APPLICATION DATA: US/09/927,180  
; FILING DATE: 09-Aug-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/519,223  
; FILING DATE: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Brown, Scott A.  
; REGISTRATION NUMBER: 32,724  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 498-8224  
; TELEFAX: (617) 876-5851  
; INFORMATION FOR SEQ ID NO: 19:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 292 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 19:  
US-09-927-180-19

Query Match 100.0%; Score 1531; DB 3; Length 292;  
Best Local Similarity 100.0%; Pred No. 4, 1e-152;  
Matches 292; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Db 1 LODLHHSRARKPAFLGSMRDKRTHDLLCLDGGVKGKGLIIIIQLLIAIEKASGVATKD 60

QY 61 LFDWVAGTSTGGILALAILHSHKSMAYMRGMYFRMKDEVRGSRPYESGPLEEFLKREFGE 120  
DB 61 LFDWVAGTSTGGILALAILHSHKSMAYMRGMYFRMKDEVRGSRPYESGPLEEFLKREFGE 120  
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DB 121 HTKMTDVRKPKVMTGTLSDRQPAELHLFRNYDAPETVREPRFNQNVNLRPPAQPSDQLV 180  
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QY 241 VSLGTGRSPQVPVTCVDVFRPSNPWELAKTVFGAKELGMVVDCCDDPGRP 292  
DB 241 VSLGTGRSPQVPVTCVDVFRPSNPWELAKTVFGAKELGMVVDCCDDPGRP 292

## RESULT 2

US-10-612-668-19  
; Sequence 19, Application US/10612668  
; Publication No. US20050196852A1  
; GENERAL INFORMATION:  
; APPLICANT: Jones, Simon  
; Tang, Jim  
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B  
; NUMBER OF SEQUENCES: 25  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genetics Institute, Inc.  
; STREET: 87 CambridgePark Drive  
; CITY: Cambridge  
; STATE: Massachusetts  
; COUNTRY: U.S.A.  
; ZIP: 02140

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/612,668  
FILING DATE: 01-Jul-2003  
CLASSIFICATION: <Unknown>

## PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/927,180  
FILING DATE: 09-Aug-2001  
APPLICATION NUMBER: 09/519,223  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Brown, Scott A.  
REGISTRATION NUMBER: 32,724  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 498-8224  
TELEFAX: (617) 876-5851  
INFORMATION FOR SEQ ID NO: 19:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 292 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 19:

US-10-612-668-19

Query Match 100.0%; Score 1531; DB 5; Length 292;  
Best Local Similarity 100.0%; Pred. No. 4.1e-152;  
Matches 292; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQDLMIHSRARKPAFILGSMRDEKRTDHLCLDGGVKGKLIIOILLIAIEKASGVATKD 60  
DB 1 LQDLMIHSRARKPAFILGSMRDEKRTDHLCLDGGVKGKLIIOILLIAIEKASGVATKD 60  
QY 61 LFDWVAGTSTGGILALAILHSHKSMAYMRGMYFRMKDEVRGSRPYESGPLEEFLKREFGE 120

DB 61 LFDWVAGTSTGGILALAILHSHKSMAYMRGMYFRMKDEVRGSRPYESGPLEEFLKREFGE 120  
QY 121 HTKMTDVRKPKVMTGTLSDRQPAELHLFRNYDAPETVREPRFNQNVNLRPPAQPSDQLV 180  
DB 121 HTKMTDVRKPKVMTGTLSDRQPAELHLFRNYDAPETVREPRFNQNVNLRPPAQPSDQLV 180  
QY 181 WRAARSSGAAPTYFRPNRFLDGGLLANNPTLDAMTEIHEYNQDLIRKQANKVKLSIV 240  
DB 181 WRAARSSGAAPTYFRPNRFLDGGLLANNPTLDAMTEIHEYNQDLIRKQANKVKLSIV 240  
QY 241 VSLGTGRSPQVPVTCVDVFRPSNPWELAKTVFGAKELGMVVDCCDDPGRP 292  
DB 241 VSLGTGRSPQVPVTCVDVFRPSNPWELAKTVFGAKELGMVVDCCDDPGRP 292

## RESULT 3

US-09-927-180-21  
; Sequence 21, Application US/09927180  
; Patent No. US20020106364A1  
; GENERAL INFORMATION:  
; APPLICANT: Jones, Simon  
; Tang, Jim  
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B  
; NUMBER OF SEQUENCES: 25  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genetics Institute, Inc.  
; STREET: 87 CambridgePark Drive  
; CITY: Cambridge  
; STATE: Massachusetts  
; COUNTRY: U.S.A.  
; ZIP: 02140

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/927,180  
FILING DATE: 09-Aug-2001  
CLASSIFICATION: <Unknown>

## PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/519,223  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Brown, Scott A.  
REGISTRATION NUMBER: 32,724  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 498-8224  
TELEFAX: (617) 876-5851  
INFORMATION FOR SEQ ID NO: 21:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 687 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 21:

US-09-927-180-21

Query Match 100.0%; Score 1531; DB 3; Length 687;  
Best Local Similarity 100.0%; Pred. No. 1.4e-151;  
Matches 292; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 396 LQDLMIHSRARKPAFILGSMRDEKRTDHLCLDGGVKGKLIIOILLIAIEKASGVATKD 455  
QY 61 LFDWVAGTSTGGILALAILHSHKSMAYMRGMYFRMKDEVRGSRPYESGPLEEFLKREFGE 120  
DB 456 LFDWVAGTSTGGILALAILHSHKSMAYMRGMYFRMKDEVRGSRPYESGPLEEFLKREFGE 515  
QY 121 HTKMTDVRKPKVMTGTLSDRQPAELHLFRNYDAPETVREPRFNQNVNLRPPAQPSDQLV 180  
DB 516 HTKMTDVRKPKVMTGTLSDRQPAELHLFRNYDAPETVREPRFNQNVNLRPPAQPSDQLV 575

GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on: March 22, 2006, 12:01:45 ; Search time 6.37555 Seconds  
(without alignments)  
1310.928 Million cell updates/sec

Title: US-10-612-668-19  
Perfect score: 1531  
Sequence: 1 LQDLMHISRAKPAFILGSM.....CAKELGKMWVDCTDPGRP 292

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 169630 seqs, 28622889 residues

Total number of hits satisfying chosen parameters: 169630

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA\_New:  
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2: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB\_pdp.\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES:

Result No.	Score	Query Match	Length	DB ID	Description
1	238	15.5	831	7 US-11-096-568A-1542	Sequence 1542, Ap
2	233	15.2	784	7 US-11-096-568A-1543	Sequence 1543, Ap
3	207	13.5	779	7 US-11-096-568A-1544	Sequence 1544, Ap
4	206.5	13.5	380	7 US-11-096-568A-3088	Sequence 3088, Ap
5	206.5	13.5	380	7 US-11-096-568A-3091	Sequence 3091, Ap
6	201	13.1	382	7 US-11-096-568A-32354	Sequence 32354, A
7	201	13.1	384	7 US-11-096-568A-32353	Sequence 32353, A
8	173	11.3	400	7 US-11-195-968-1	Sequence 1, Appli
9	155.5	10.2	406	7 US-11-195-968-12	Sequence 12, Appl
10	147	9.6	526	7 US-11-096-568A-34163	Sequence 34163, A
11	138.5	9.0	297	7 US-11-096-568A-3089	Sequence 3089, Ap
12	132.5	8.7	288	7 US-11-096-568A-32355	Sequence 32355, A
13	129.5	8.5	391	7 US-11-058-727-123	Sequence 123, App
14	129.5	8.5	391	7 US-11-108-389-123	Sequence 123, App
15	129.5	8.5	391	7 US-11-224-624-123	Sequence 123, App
16	125	8.2	391	7 US-11-058-727-119	Sequence 119, App
17	125	8.2	391	7 US-11-058-727-121	Sequence 121, App
18	125	8.2	391	7 US-11-108-389-119	Sequence 119, App
19	125	8.2	391	7 US-11-108-389-121	Sequence 121, App
20	125	8.2	391	7 US-11-224-624-119	Sequence 119, App
21	125	8.2	391	7 US-11-224-624-121	Sequence 121, App
22	124.5	8.1	249	7 US-11-096-568A-3090	Sequence 3090, Ap
23	122.5	8.0	454	7 US-11-096-568A-18178	Sequence 18178, A
24	122.5	8.0	460	7 US-11-096-568A-18177	Sequence 18177, A
25	117	7.6	396	7 US-11-096-568A-34164	Sequence 34164, A

26	111.5	7.3	381	7 US-11-096-568A-34165	Sequence 34165, A
27	85	5.6	467	7 US-11-072-512-2838	Sequence 2838, Ap
28	84.5	5.5	348	7 US-11-087-099-10729	Sequence 10729, A
29	84	5.5	360	7 US-11-096-568A-27737	Sequence 27737, A
30	84	5.5	394	7 US-11-096-568A-27736	Sequence 27736, A
31	84	5.5	482	7 US-11-096-568A-27735	Sequence 27735, A
32	83	5.4	591	7 US-11-098-686-11119	Sequence 11119, A
33	82	5.4	558	6 US-10-467-657-4258	Sequence 4258, Ap
34	81.5	5.3	619	7 US-11-210-471-4	Sequence 4, Appli
35	80.5	5.3	619	7 US-11-210-471-10	Sequence 10, Appl
36	80.5	5.3	3588	6 US-10-995-561-672	Sequence 672, App
37	80.5	5.3	4346	6 US-10-995-561-671	Sequence 671, App
38	80.5	5.3	4347	6 US-10-995-561-670	Sequence 670, App
39	80.5	5.3	4390	7 US-11-169-041-169	Sequence 169, App
40	80.5	5.3	4419	6 US-10-821-234-1155	Sequence 1155, Ap
41	79.5	5.2	330	7 US-11-087-059-8291	Sequence 8291, Ap
42	79	5.2	228	7 US-11-052-554A-366	Sequence 366, App
43	79	5.2	359	6 US-10-467-657-1650	Sequence 1650, Ap
44	79	5.2	1377	6 US-10-821-234-1070	Sequence 1070, Ap
45	78.5	5.1	310	7 US-11-096-568A-27488	Sequence 27488, A

ALIGNMENTS

RESULT 1  
US-11-096-568A-1542  
; Sequence 1542, Application US/11096568A  
; Publication No. US20060048240A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexandrov, Nikolai et al.  
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptide  
; TITLE OF INVENTION: Therby  
; FILE REFERENCE: 2750-1592PUS2  
; CURRENT APPLICATION NUMBER: US/11/096,568A  
; CURRENT FILING DATE: 2005-04-01  
; NUMBER OF SEQ ID NOS: 34471  
; SEQ ID NO 1542  
; LENGTH: 831  
; TYPE: PRT  
; ORGANISM: Zea mays subsp. mays  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)..(831)  
; OTHER INFORMATION: Ceres Seq. ID no. 14313476  
US-11-096-568A-1542

Query Match	15.5%	Score 238;	DB 7;	Length 831;
Best Local Similarity	26.8%	Pred. No. 6.8e-15;		
Matches	77;	Conservative 40;	Mismatches 84;	Indels 86;
Gaps	10;			
QY	30	LLCLDGGVKGIIIIQLLIAIEKASGVATKDLFDWAGTSTGGILALAI-LHKSMAVMR	88	
Db	45	ILSMDDGGMKGLATVQMLKQIEQGTGKRHEMFDLIGTSTGGMLMALGDKQMTLDQCE	104	
QY	89	GMVFRM-----KDE-----VFRGSRVYESGPLEEFLKR-	116	
Db	105	EITTKLGLVFAPIPKDEATWKEKDLQLFKSSSSQFRVVVHGSK-HSADQFERLLKEM	163	
QY	117	---EFGHTKMTDVRK-PKVMLTGTLSDRQPAELHLFRNYDAPETVREPRFNQMVNRPP	172	
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QY	173	AQPSDQI-----WRAARSSGAAPTYFR-----PNGRFLD	202	
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QY	203	GGLANNPTLDAMTETHEYNQDLIRKGOANKVKLSLVVSLGTGRSP	249	
Db	276	GAIVANNPTIFAIREAQLLPD-----TRIDCLVSGCGSVP	312	

RESULT 2



GenCore version 5.1.7  
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OM.protein - protein search, using sw model

Run on: March 22, 2006, 11:25:51 ; Search time 15.1596 Seconds  
(without alignments)  
1592.473 Million cell updates/sec

Title: US-10-612-668-19  
Perfect score: 1531  
Sequence: 1 LQDLMHISRAKPAFLIGSM.....GAKELGRVVDCTDPDGRP 292

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.\*

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- 2: /cgn2\_6/ptodata/1/iaa/6\_COMB.pep.\*
- 3: /cgn2\_6/ptodata/1/iaa/H\_COMB.pep.\*
- 4: /cgn2\_6/ptodata/1/iaa/PTUS\_COMB.pep.\*
- 5: /cgn2\_6/ptodata/1/iaa/RE\_COMB.pep.\*
- 6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1531	100.0	292	1	US-08-555-568B-19
2	1531	100.0	292	2	US-09-519-223-19
3	1531	100.0	292	2	US-09-927-180-19
4	1531	100.0	687	1	US-08-555-568B-21
5	1531	100.0	687	2	US-09-519-223-21
6	1531	100.0	687	2	US-09-927-180-21
7	1531	100.0	688	1	US-08-555-568B-23
8	1531	100.0	688	2	US-09-519-223-23
9	1531	100.0	688	2	US-09-927-180-23
10	1524	99.5	819	2	US-09-949-016-10948
11	1471	96.1	752	1	US-08-281-193-2
12	1471	96.1	752	1	US-08-422-106-2
13	1471	96.1	752	1	US-08-735-716-2
14	1471	96.1	752	1	US-08-555-568B-2
15	1471	96.1	752	1	US-09-519-223-2
16	1471	96.1	752	2	US-09-927-180-2
17	1471	96.1	752	4	PCT-US95-08069-2
18	736	48.1	896	2	US-09-270-767-46130
19	610	39.8	545	2	US-09-270-767-61684
20	371	24.2	143	2	US-09-270-767-33298
21	177	11.6	410	2	US-09-755-630B-290
22	177	11.6	410	2	US-09-755-630B-292
23	177	11.6	410	2	US-09-755-274-10
24	177	11.6	410	2	US-09-755-274-12
25	177	11.6	410	2	US-10-658-180-290
26	177	11.6	410	2	US-10-658-180-292
27	175	11.4	337	2	US-09-755-630B-293

28	175	11.4	337	2	US-09-755-274-13	Sequence 13, Appl
29	175	11.4	337	2	US-10-658-180-293	Sequence 293, App
30	175	11.4	410	1	US-08-449-986-2	Sequence 2, Appli
31	175	11.4	410	1	US-08-756-855-2	Sequence 2, Appli
32	175	11.4	410	2	US-09-755-630B-288	Sequence 288, App
33	175	11.4	410	2	US-09-755-630B-291	Sequence 291, App
34	175	11.4	410	2	US-09-755-274-8	Sequence 8, Appli
35	175	11.4	410	2	US-09-755-274-11	Sequence 11, Appl
36	175	11.4	410	2	US-10-658-180-288	Sequence 288, App
37	175	11.4	410	2	US-10-658-180-291	Sequence 291, App
38	175	11.4	508	2	US-09-755-630B-289	Sequence 289, App
39	175	11.4	508	2	US-09-755-274-9	Sequence 9, Appli
40	175	11.4	508	2	US-10-658-180-289	Sequence 289, App
41	142.5	9.3	383	1	US-07-936-163-4	Sequence 4, Appli
42	140	9.1	381	1	US-07-936-163-3	Sequence 3, Appli
43	140	9.1	386	2	US-09-755-630B-278	Sequence 278, App
44	140	9.1	386	2	US-09-755-274-5	Sequence 5, Appli
45	140	9.1	386	2	US-10-658-180-278	Sequence 278, App

ALIGNMENTS

RESULT 1  
US-08-555-568B-19  
; Sequence 19, Application US/08555568B  
; Patent No. 5976854  
; GENERAL INFORMATION:  
; APPLICANT: Jones, Simon  
; APPLICANT: Tang, Jim  
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B  
; NUMBER OF SEQUENCES: 25  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genetics Institute, Inc.  
; STREET: 87 Cambridgepark Drive  
; CITY: Cambridge  
; STATE: Massachusetts  
; COUNTRY: U.S.A.  
; ZIP: 02140  
; COMPUTER READABLE FORM: disk  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25 (BPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/555,568B  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Brown, Scott A.  
; REGISTRATION NUMBER: 32,724  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 498-8224  
; TELEFAX: (617) 876-5851  
; INFORMATION FOR SEQ ID NO: 19:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 292 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-555-568B-19

Query Match	100.0%;	Score 1531;	DB 1;	Length 292;
Best Local Similarity	100.0%;	Pred. No. 2.4e-167;		
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Db	1	LQDLMHISRAKPAFLIGSMRDEKTRHLLCLDGGVKGKGLIIQLLIAIEKASGVATKD	60	
QY	61	LFDWAGTGTGILAILHLKSMAYMRGMVFRMKDEVFRGSPYSGPLEEFLKREFGE	120	
Db	61	LFDWAGTGTGILAILHLKSMAYMRGMVFRMKDEVFRGSPYSGPLEEFLKREFGE	120	

QY 121 HTKMTDVRKPKVMTCTLSDRQPAELHLFRNYDAPETVREPRFNQNVNLRPPAQSDQLV 180  
Db 121 HTKMTDVRKPKVMTCTLSDRQPAELHLFRNYDAPETVREPRFNQNVNLRPPAQSDQLV 180  
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QY 241 VSLGTGRSPQVPVTCVDVFRPSNPWELAKTVFGAKELGKMVVDCCCTDPDGRP 292  
Db 241 VSLGTGRSPQVPVTCVDVFRPSNPWELAKTVFGAKELGKMVVDCCCTDPDGRP 292

RESULT 2

US-09-519-223-19  
; Sequence 19, Application US/09519223  
; Patent No. 6274140  
; GENERAL INFORMATION:  
; APPLICANT: Jones, Simon  
; APPLICANT: Tang, Jim  
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B  
; NUMBER OF SEQUENCES: 25  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genetics Institute, Inc.  
; STREET: 87 CambridgePark Drive  
; CITY: Cambridge  
; STATE: Massachusetts  
; COUNTRY: U.S.A.  
; ZIP: 02140  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.25 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/519,223  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/555,568  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Brown, Scott A.  
; REGISTRATION NUMBER: 32,724  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 498-8224  
; TELEFAX: (617) 876-5851  
; INFORMATION FOR SEQ ID NO: 19:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 292 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-519-223-19

Query Match 100.0%; Score 1531; DB 2; Length 292;  
Best Local Similarity 100.0%; Pred. No. 2.4e-167;  
Matches 292; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 LQDLMHISRARKPAFILGSMRDEKTRTHDHLCLDGGVKGKLIILQLLIAIEKASGVATKD 60  
Db 1 LQDLMHISRARKPAFILGSMRDEKTRTHDHLCLDGGVKGKLIILQLLIAIEKASGVATKD 60  
QY 61 LFDWVAGTSTGGILALAILHLSKSMAYMRGMVFRMKDEVFGRSGRPYESGPLEEFLKREFGE 120  
Db 61 LFDWVAGTSTGGILALAILHLSKSMAYMRGMVFRMKDEVFGRSGRPYESGPLEEFLKREFGE 120  
QY 121 HTKMTDVRKPKVMTCTLSDRQPAELHLFRNYDAPETVREPRFNQNVNLRPPAQSDQLV 180  
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Db 181 WRAARSSGAAPTYFRPNRFLDGLLANNPTLDAMTEIHEYNQDLIRKQANKVKLSIV 240  
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RESULT 3  
US-09-927-180-19  
; Sequence 19, Application US/09927180  
; Patent No. 6645736  
; GENERAL INFORMATION:  
; APPLICANT: Jones, Simon  
; APPLICANT: Tang, Jim  
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B  
; NUMBER OF SEQUENCES: 25  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genetics Institute, Inc.  
; STREET: 87 CambridgePark Drive  
; CITY: Cambridge  
; STATE: Massachusetts  
; COUNTRY: U.S.A.  
; ZIP: 02140  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.25 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/927,180  
; FILING DATE: 09-Aug-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/519,223  
; FILING DATE: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Brown, Scott A.  
; REGISTRATION NUMBER: 32,724  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 498-8224  
; TELEFAX: (617) 876-5851  
; INFORMATION FOR SEQ ID NO: 19:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 292 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 19:  
US-09-927-180-19  
Query Match 100.0%; Score 1531; DB 2; Length 292;  
Best Local Similarity 100.0%; Pred. No. 2.4e-167;  
Matches 292; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 LQDLMHISRARKPAFILGSMRDEKTRTHDHLCLDGGVKGKLIILQLLIAIEKASGVATKD 60  
Db 1 LQDLMHISRARKPAFILGSMRDEKTRTHDHLCLDGGVKGKLIILQLLIAIEKASGVATKD 60  
QY 61 LFDWVAGTSTGGILALAILHLSKSMAYMRGMVFRMKDEVFGRSGRPYESGPLEEFLKREFGE 120  
Db 61 LFDWVAGTSTGGILALAILHLSKSMAYMRGMVFRMKDEVFGRSGRPYESGPLEEFLKREFGE 120  
QY 121 HTKMTDVRKPKVMTCTLSDRQPAELHLFRNYDAPETVREPRFNQNVNLRPPAQSDQLV 180  
Db 121 HTKMTDVRKPKVMTCTLSDRQPAELHLFRNYDAPETVREPRFNQNVNLRPPAQSDQLV 180  
QY 181 WRAARSSGAAPTYFRPNRFLDGLLANNPTLDAMTEIHEYNQDLIRKQANKVKLSIV 240  
Db 181 WRAARSSGAAPTYFRPNRFLDGLLANNPTLDAMTEIHEYNQDLIRKQANKVKLSIV 240  
QY 241 VSLGTGRSPQVPVTCVDVFRPSNPWELAKTVFGAKELGKMVVDCCCTDPDGRP 292

GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: March 22, 2006, 12:00:11 ; Search time 120 Seconds  
(without alignments)

2392.073 Million cell updates/sec

Title: US-10-612-668-21

Perfect score: 3620

Sequence: 1 MQFFGLVNTFSGVTLNFSN.....GAKELGRWVDDCTDPDGRP 687

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA Main:  
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2: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep:\*  
3: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep:\*  
4: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep:\*  
5: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep:\*  
6: /cgn2\_6/ptodata/1/pubpaa/US11\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3620	100.0	687	3	US-09-927-180-21
2	3620	100.0	687	5	US-10-612-668-21
3	3606.5	99.6	688	3	US-09-927-180-23
4	3606.5	99.6	688	5	US-10-612-668-23
5	3302.5	91.2	752	3	US-09-927-180-2
6	3302.5	91.2	752	5	US-10-612-668-2
7	2723	75.2	667	4	US-10-108-260A-3778
8	2084	57.6	394	3	US-09-927-180-17
9	2084	57.6	394	5	US-10-612-668-17
10	1531	42.3	292	3	US-09-927-180-19
11	1531	42.3	292	5	US-10-612-668-19
12	1163.5	32.1	877	6	US-11-097-143-14664
13	647.5	17.9	1071	4	US-10-369-493-6865
14	634.5	17.5	1023	4	US-10-369-493-6689
15	634.5	17.5	1023	4	US-10-369-493-6690
16	324.5	9.0	468	4	US-10-369-493-4998
17	324	9.0	1330	4	US-10-108-260A-3237
18	320	8.8	1549	6	US-11-097-143-1776
19	320	8.8	1549	6	US-11-097-143-29028
20	302.5	8.4	2443	6	US-11-097-143-8355
21	302	8.3	786	4	US-10-164-080-2
22	302	8.3	786	4	US-10-299-327-2
23	302	8.3	786	4	US-10-128-174-13
24	302	8.3	786	4	US-10-128-174-31
25	302	8.3	786	4	US-10-128-174-32
26	302	8.3	786	4	US-10-128-174-33
27	302	8.3	787	3	US-09-866-050A-334

28 301.5 8.3 347 4 US-10-128-174-30 Sequence 30, Appl  
29 300.5 8.3 1724 3 US-09-964-899-43 Sequence 43, Appl  
30 300.5 8.3 1724 5 US-10-975-523-43 Sequence 43, Appl  
31 300 8.3 1762 4 US-10-205-194-117 Sequence 117, Appl  
32 296 8.2 1094 5 US-10-479-764-22 Sequence 22, Appl  
33 296 8.2 1097 5 US-10-450-763-52300 Sequence 52300, A  
34 296 8.2 3913 4 US-10-334-143-45 Sequence 45, Appl  
35 296 8.2 4274 5 US-10-450-763-31331 Sequence 31331, A  
36 296 8.2 4377 5 US-10-756-149-4917 Sequence 4917, Ap  
37 296 8.2 4386 5 US-10-450-763-37734 Sequence 37734, A  
38 296 8.2 4397 5 US-10-450-763-52303 Sequence 52303, A  
39 290 8.0 720 4 US-10-433-794-20 Sequence 20, Appl  
40 290 8.0 765 4 US-10-128-174-3 Sequence 3, Appl  
41 290 8.0 765 4 US-10-128-174-34 Sequence 34, Appl  
42 290 8.0 765 4 US-10-128-174-35 Sequence 35, Appl  
43 290 8.0 765 4 US-10-128-174-36 Sequence 36, Appl  
44 290 8.0 785 4 US-10-128-174-37 Sequence 37, Appl  
45 290 8.0 765 4 US-10-128-174-38 Sequence 38, Appl

#### ALIGNMENTS

#### RESULT 1

US-09-927-180-21  
; Sequence 21, Application US/09927180  
; Patent No. US20020106364A1  
; GENERAL INFORMATION:  
; APPLICANT: Tang, Jim  
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B  
; NUMBER OF SEQUENCES: 25  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genetics Institute, Inc.  
; STREET: 87 CambridgePark Drive  
; CITY: Cambridge  
; STATE: Massachusetts  
; COUNTRY: U.S.A.  
; ZIP: 02140  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)  
; CURRENT APPLICATION DATA: US/09/927,180  
; APPLICATION NUMBER: US/09/927,180  
; FILING DATE: 09-Aug-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/519,223  
; FILING DATE: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Brown, Scott A.  
; REGISTRATION NUMBER: 32,724  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 498-8224  
; TELEFAX: (617) 876-5851  
; INFORMATION FOR SEQ ID NO: 21:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 687 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 21:  
US-09-927-180-21

Query Match 100.0%; Score 3620; DB 3; Length 687;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 687; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQFFGLVNTFSGVTLNFSNPRVKEVAADYTTSSDRVREEGQLILFQNTPNRTWDCVLV 60

DB 1 MQFFGLVNTFSGVTLNFSNPRVKEVAADYTTSSDRVREEGQLILFQNTPNRTWDCVLV 60

QY 61 NPRNSQSGRLFOLEADALVNFHQYSSQLLPFYESSPOVLHTEVLQHLTDLIRNHPW 120  
DB 61 NPRNSQSGRLFOLEADALVNFHQYSSQLLPFYESSPOVLHTEVLQHLTDLIRNHPW 120  
QY 121 SVAHLAVELGIRECFHSHRIISCANCAENEBEGCTPLHLACRKGDEILVELVQYCHTQMD 180  
DB 121 SVAHLAVELGIRECFHSHRIISCANCAENEBEGCTPLHLACRKGDEILVELVQYCHTQMD 180  
QY 181 VTDYKGETVHYAVQGNDSQVQLLGRNAVAGLNVNNOGLTPLHLACOLGQEMVRVLL 240  
DB 181 VTDYKGETVHYAVQGNDSQVQLLGRNAVAGLNVNNOGLTPLHLACOLGQEMVRVLL 240  
QY 241 LCNARCNIMGPNGYPIHSAMKFSQKCAEMIISMDSSQIHSKDPYRGASPLHWAKNAEMA 300  
DB 241 LCNARCNIMGPNGYPIHSAMKFSQKCAEMIISMDSSQIHSKDPYRGASPLHWAKNAEMA 300  
QY 301 RMLLKRCNCNVNSTSSAGNTALHVGVMNRNFDCAIIVLLTHGANADARGEHNTPLHLAMSK 360  
DB 301 RMLLKRCNCNVNSTSSAGNTALHVGVMNRNFDCAIIVLLTHGANADARGEHNTPLHLAMSK 360  
QY 361 DNVEMIKALIVFGAEDVTPNDFGETPTFLASKIGKQLDLMHISRARKPAFILGSMRDEKR 420  
DB 361 DNVEMIKALIVFGAEDVTPNDFGETPTFLASKIGKQLDLMHISRARKPAFILGSMRDEKR 420  
QY 421 THDHLCLDGGVGKGLIIIOQLLIAIEKASGVATKDLFDWVAGTSTGGILALAILHKSMA 480  
DB 421 THDHLCLDGGVGKGLIIIOQLLIAIEKASGVATKDLFDWVAGTSTGGILALAILHKSMA 480  
QY 481 YNRGMYFRMKDEVFRGSRPYESGPLEEFKREFGEHTKMTDVRKPKVMTGTLSDRQPAE 540  
DB 481 YNRGMYFRMKDEVFRGSRPYESGPLEEFKREFGEHTKMTDVRKPKVMTGTLSDRQPAE 540  
QY 541 LHLFRNYDAPETVREPRFNQNVNLRPPAQPDSQOLVWRAARSSGAAPTYFRPNRGRFLDGG 600  
DB 541 LHLFRNYDAPETVREPRFNQNVNLRPPAQPDSQOLVWRAARSSGAAPTYFRPNRGRFLDGG 600  
QY 601 LANNPTLDAMTEIHEYNDLIRKQANKVKLSIVVSLGTGRSPQVPTCDVFRPSNPW 660  
DB 601 LANNPTLDAMTEIHEYNDLIRKQANKVKLSIVVSLGTGRSPQVPTCDVFRPSNPW 660  
QY 661 ELAKTVFGAKELGKMVDDCCTDPDGRP 687  
DB 661 ELAKTVFGAKELGKMVDDCCTDPDGRP 687

## RESULT 2

US-10-612-668-21

Sequence 21, Application US/10612668

Publication No. US20050196852A1

GENERAL INFORMATION:

APPLICANT: Jones, Simon

Tang, Jim

TITLE OF INVENTION: Calcium Independent Phospholipase A2/B

NUMBER OF SEQUENCES: 25

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genetics Institute, Inc.

STREET: 87 Cambridge Park Drive

CITY: Cambridge

STATE: Massachusetts

COUNTRY: U.S.A.

ZIP: 02140

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA: US/10/612,668

APPLICATION NUMBER: US/10/612,668

FILING DATE: 01-Jul-2003

CLASSIFICATION: &lt;Unknown&gt;

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/927,180

FILING DATE: 09-Aug-2001

APPLICATION NUMBER: 09/519,223

FILING DATE: &lt;Unknown&gt;

ATTORNEY/AGENT INFORMATION:

NAME: Brown, Scott A.

REGISTRATION NUMBER: 32,724

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 498-8224

TELEFAX: (617) 876-5851

INFORMATION FOR SEQ ID NO: 21:

SEQUENCE CHARACTERISTICS:

LENGTH: 687 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 21:

US-10-612-668-21

Query Match 100.0%; Score 3620; DB 5; Length 687;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 687; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MOFFGRLVNTFGVNTLFSNPRVKEVAVADYTSRVRREEGQLILFQNTPNRTWDCVLV 60  
DB 1 MOFFGRLVNTFGVNTLFSNPRVKEVAVADYTSRVRREEGQLILFQNTPNRTWDCVLV 60  
QY 61 NPNRSQSGRLFOLEADALVNFHQYSSQLLPFYESSPOVLHTEVLQHLTDLIRNHPW 120  
DB 61 NPNRSQSGRLFOLEADALVNFHQYSSQLLPFYESSPOVLHTEVLQHLTDLIRNHPW 120  
QY 121 SVAHLAVELGIRECFHSHRIISCANCAENEBEGCTPLHLACRKGDEILVELVQYCHTQMD 180  
DB 121 SVAHLAVELGIRECFHSHRIISCANCAENEBEGCTPLHLACRKGDEILVELVQYCHTQMD 180  
QY 181 VTDYKGETVHYAVQGNDSQVQLLGRNAVAGLNVNNOGLTPLHLACOLGQEMVRVLL 240  
DB 181 VTDYKGETVHYAVQGNDSQVQLLGRNAVAGLNVNNOGLTPLHLACOLGQEMVRVLL 240  
QY 241 LCNARCNIMGPNGYPIHSAMKFSQKCAEMIISMDSSQIHSKDPYRGASPLHWAKNAEMA 300  
DB 241 LCNARCNIMGPNGYPIHSAMKFSQKCAEMIISMDSSQIHSKDPYRGASPLHWAKNAEMA 300  
QY 301 RMLLKRCNCNVNSTSSAGNTALHVGVMNRNFDCAIIVLLTHGANADARGEHNTPLHLAMSK 360  
DB 301 RMLLKRCNCNVNSTSSAGNTALHVGVMNRNFDCAIIVLLTHGANADARGEHNTPLHLAMSK 360  
QY 361 DNVEMIKALIVFGAEDVTPNDFGETPTFLASKIGKQLDLMHISRARKPAFILGSMRDEKR 420  
DB 361 DNVEMIKALIVFGAEDVTPNDFGETPTFLASKIGKQLDLMHISRARKPAFILGSMRDEKR 420  
QY 421 THDHLCLDGGVGKGLIIIOQLLIAIEKASGVATKDLFDWVAGTSTGGILALAILHKSMA 480  
DB 421 THDHLCLDGGVGKGLIIIOQLLIAIEKASGVATKDLFDWVAGTSTGGILALAILHKSMA 480  
QY 481 YNRGMYFRMKDEVFRGSRPYESGPLEEFKREFGEHTKMTDVRKPKVMTGTLSDRQPAE 540  
DB 481 YNRGMYFRMKDEVFRGSRPYESGPLEEFKREFGEHTKMTDVRKPKVMTGTLSDRQPAE 540  
QY 541 LHLFRNYDAPETVREPRFNQNVNLRPPAQPDSQOLVWRAARSSGAAPTYFRPNRGRFLDGG 600  
DB 541 LHLFRNYDAPETVREPRFNQNVNLRPPAQPDSQOLVWRAARSSGAAPTYFRPNRGRFLDGG 600  
QY 601 LANNPTLDAMTEIHEYNDLIRKQANKVKLSIVVSLGTGRSPQVPTCDVFRPSNPW 660  
DB 601 LANNPTLDAMTEIHEYNDLIRKQANKVKLSIVVSLGTGRSPQVPTCDVFRPSNPW 660  
QY 661 ELAKTVFGAKELGKMVDDCCTDPDGRP 687  
DB 661 ELAKTVFGAKELGKMVDDCCTDPDGRP 687

## RESULT 3

US-09-927-180-23

GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 22, 2006, 12:01:45 ; Search time 15 Seconds  
(without alignments)  
1310.928 Million cell updates/sec

Title: US-10-612-668-21

Perfect score: 3620

Sequence: 1 MQPFGRLWNTSGVTNLFN.....GAKELGKVVDCCTDPGRP 687

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 169630 seqs, 28622889 residues

Total number of hits satisfying chosen parameters: 169630

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA New:

- 1: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB\_PEP.\*
- 2: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB\_PEP.\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB\_PEP.\*
- 4: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB\_PEP.\*
- 5: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB\_PEP.\*
- 6: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB\_PEP.\*
- 7: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB\_PEP.\*
- 8: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB\_PEP.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	310	8.6	1159	6	US-10-055-877-139
2	296	8.2	4384	6	US-10-821-234-1120
3	294.5	8.1	1765	6	US-10-055-877-140
4	294.5	8.1	1940	6	US-10-055-877-141
5	279.5	7.7	784	7	US-11-072-175-153
6	278.5	7.7	1059	6	US-10-055-877-138
7	264	7.3	1431	6	US-10-501-035-220
8	251.5	6.9	795	7	US-11-072-512-2378
9	249	6.9	791	6	US-10-055-877-137
10	244	6.7	237	7	US-11-096-568A-28113
11	244	6.7	247	7	US-11-096-568A-28112
12	238	6.6	247	7	US-11-096-568A-28112
13	234	6.5	993	6	US-11-096-568A-1542
14	233	6.4	784	7	US-11-096-568A-1543
15	230	6.4	645	7	US-11-072-512-2588
16	229.5	6.3	240	7	US-11-096-568A-22417
17	229.5	6.3	244	7	US-11-096-568A-22416
18	225.5	6.2	505	7	US-11-072-512-2553
19	223	6.2	219	7	US-11-096-568A-28114
20	215	5.9	241	7	US-11-096-568A-9945
21	215	5.9	245	7	US-11-096-568A-9944
22	215	5.9	280	7	US-11-096-568A-9943
23	215	5.9	2556	7	US-11-050-346-67
24	210	5.8	1719	7	US-11-234-786-378
25	209.5	5.8	656	7	US-11-234-786-379

26	209.5	5.8	671	7	US-11-234-786-380
27	208.5	5.8	657	7	US-11-072-512-2529
28	208.5	5.8	835	7	US-11-186-283-2
29	207	5.7	779	7	US-11-096-568A-1544
30	206.5	5.7	380	7	US-11-096-568A-3088
31	206.5	5.7	835	7	US-11-096-568A-3091
32	206.5	5.7	2471	7	US-11-186-283-8
33	205	5.7	329	7	US-11-050-346-68
34	202	5.6	382	7	US-11-234-786-376
35	201	5.6	384	7	US-11-096-568A-32354
36	201	5.6	384	7	US-11-096-568A-32353
37	197	5.4	292	7	US-11-234-786-532
38	196.5	5.4	596	7	US-11-072-512-2675
39	194	5.4	1554	7	US-11-186-284-93
40	190.5	5.3	456	7	US-11-096-568A-16313
41	190.5	5.3	461	7	US-11-096-568A-16312
42	185.5	5.1	433	7	US-11-096-568A-11369
43	185.5	5.1	436	7	US-11-096-568A-11368
44	185.5	5.1	448	7	US-11-096-568A-11367
45	180	5.0	504	7	US-11-096-568A-10314

#### ALIGNMENTS

#### RESULT 1

US-10-055-877-139  
Sequence 139, Application US/10055877  
Publication No. US20050288241A1  
GENERAL INFORMATION:  
APPLICANT: DeCristofaro, Marc  
APPLICANT: Padigaru, Muralidhara  
APPLICANT: Miller, Charles  
APPLICANT: Tchernev, Velizar  
APPLICANT: Zhong, Mei  
APPLICANT: Anderson, David  
APPLICANT: Ballinger, Robert  
APPLICANT: Gerlach, Valerie  
APPLICANT: Spytek, Kimberly  
APPLICANT: Ratelli, Luca  
APPLICANT: Kekuda, Ramesh  
APPLICANT: Guo, Xiaojia  
APPLICANT: Zerhusen, Bryan  
APPLICANT: Andrew, David  
APPLICANT: Mezes, Peter  
APPLICANT: Patturajan, Meera  
APPLICANT: Burgess, Catherine  
APPLICANT: Eisen, Andrew  
APPLICANT: Wolenc, Adam  
APPLICANT: Baumgartner, Jason  
APPLICANT: Shimkets, Richard  
APPLICANT: Gusev, Vladimir  
APPLICANT: Vernet, Corine  
APPLICANT: Taupier Jr., Raymond  
APPLICANT: Pena, Carol  
APPLICANT: Shenoy, Suresh  
APPLICANT: Li, Li  
APPLICANT: Casman, Stacie  
APPLICANT: Boldog, Ferenc  
TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoded Thereby  
FILE REFERENCE: 21402-251  
CURRENT APPLICATION NUMBER: US/10/055,877  
CURRENT FILING DATE: 2002-01-22  
PRIOR APPLICATION NUMBER: 60/262,892  
PRIOR FILING DATE: 2001-01-19  
PRIOR APPLICATION NUMBER: 60/263,598  
PRIOR FILING DATE: 2001-01-23  
PRIOR APPLICATION NUMBER: 60/263,799  
PRIOR FILING DATE: 2001-01-24  
PRIOR APPLICATION NUMBER: 60/264,117  
PRIOR FILING DATE: 2001-01-25  
PRIOR APPLICATION NUMBER: 60/264,139  
PRIOR FILING DATE: 2001-01-25

PRIOR APPLICATION NUMBER: 60/264,478  
PRIOR FILING DATE: 2001-01-26  
PRIOR APPLICATION NUMBER: 60/263,351  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: 60/272,870  
PRIOR FILING DATE: 2001-03-02  
PRIOR APPLICATION NUMBER: 60/275,990  
PRIOR FILING DATE: 2001-03-14  
PRIOR APPLICATION NUMBER: 60/275,927  
PRIOR FILING DATE: 2001-03-14  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 512  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 139  
LENGTH: 1159  
TYPE: PRT  
ORGANISM: Drosophila melanogaster  
US-10-055-877-139

Query Match 8.6%; Score 310; DB 6; Length 1159;  
Best Local Similarity 27.8%; Pred. No. 1.1e-19;  
Matches 95; Conservative 64; Mismatches 117; Indels 66; Gaps 11;

QY 103 HTEVLQHLTDLIRNHS-----NSVAHLA-----VELGIRCFHHSRIISCANCA 147  
DB 349 HVRVAKLLLD--RNADANARALNGFTPLHIAKKNRLKVVELLRL---HGASIS---A 398  
QY 148 ENEEGCTTPLHLACRKGDELVELVOYCHTQMDVTDYKGETVPHYAVQGDNSQVQLQGR 207  
DB 399 TTESGUTPLHVAAFMGCMNIVVYLQH--DASPDVPTVGETPLHIAARANQTDIIIRLLR 457  
QY 208 NAVAGLNQVNNQGLTPLHLACQLGKQEMVRVLLLCNARGN-----247  
DB 458 NG-AQVDARAREQQTPLHIASRLGNVDIVMLLQHGQVDATTKDMYTALHIAAKEGQDE 516  
QY 248 ---IMPNG-----YPIHSAMKFSQKCAEMIISMDSQIHSKDPHYGASPLHW 293  
DB 517 VAAVLIENGAAALDAATKKGFTPLHLTAKYGHKIVQAQLLQKEADV--DAQGKNGVTPHLV 574  
QY 294 A---KNAEWARMLLKGCNNVNSTSSAGNTALHVGVMNRFDCAIVLLTHGANADARGEHG 350  
DB 575 ACHYNNQVALLLEKLGASPHATKNGHTPLHIAARKNQMDIATTLLEYGALANAEKAG 634  
QY 351 NTPHLAMSKDNVEMIKALIVFGAEVDTNDFTGFTTFLASK 392  
DB 635 FTPLHLSQEGRAEINLLIEHKAAVNHPAKNGLTTPMHLCAQ 676

RESULT 2  
US-10-821-234-1120  
Sequence 1120, Application US/10821234  
Publication No. US20050255114A1  
GENERAL INFORMATION:  
APPLICANT: Labat, Ivan  
APPLICANT: Stache-Crain, Birgit  
APPLICANT: Andarmani, Susan  
APPLICANT: Tang, Y. Tom  
TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia  
FILE REFERENCE: 821A  
CURRENT APPLICATION NUMBER: US/10/821,234  
CURRENT FILING DATE: 2004-04-07  
PRIOR APPLICATION NUMBER: US 60/462,047  
PRIOR FILING DATE: 2003-04-07  
NUMBER OF SEQ ID NOS: 1704  
SOFTWARE: pt\_seq\_genes Version 1.0  
SEQ ID NO 1120  
LENGTH: 4384  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-821-234-1120

Query Match 8.2%; Score 296; DB 6; Length 4384;  
Best Local Similarity 29.2%; Pred. No. 1.7e-17;

Matches 81; Conservative 54; Mismatches 130; Indels 12; Gaps 6;  
QY 124 HLAVELGIRECFHHSRIISCANCAENEECTPLHLACRKGDELVELVOYCHTQMDVTD 183  
DB 511 HISARLGKADIVQQLLOQASPNAAATTSYTPHLHLSAREGHEDVAAFLDHH--GASUSITT 569  
QY 184 YKGETVPHYAVQGDNSQVQLQGRNAVAGLNQVNNQGLTPLHLACQLGKQEMVRVLLLCN 243  
DB 570 KKGFTPLHVAAYKGLKLEAVANLLQKS--ASPDAAAGSKGLTPLHVAAHYDNQKVALLLDQ 628  
QY 244 ARCNTMGPNY-PIHSAMKFSQKCAEMI--SMDSQIHSKDPHYGASPLHWAK---NA 297  
DB 629 ASPHAAAKNGYTPHLHIAKKNQMDIATTLLEYGADANAV---TROGSIASVHLAAQEGHV 684  
QY 298 EMARMLLKGCNNVNSTSSAGNTALHVGVMNRFDCAIVLLTHGANADARGEHGNTPLHLA 357  
DB 685 DMVSILLGRNANVNLNKSGLTPLHLAAQEDRVNVAEVLVNOGHVDAQTCKMGTTPHLVG 744  
QY 358 MSKDNVEMIKALIVFGAEVDTNDFTGFTTFLASKIG 394.  
DB 745 CHYGNIKIVNFWLQHSKAKVNAKTKNGYTPHLHQAQOG 781

RESULT 3  
US-10-055-877-140  
Sequence 140, Application US/10055877  
Publication No. US20050288241A1  
GENERAL INFORMATION:  
APPLICANT: DeCristofaro, Marc  
APPLICANT: Padigaru, Muralidhara  
APPLICANT: Miller, Charles  
APPLICANT: Tchernev, Velizar  
APPLICANT: Zhong, Mei  
APPLICANT: Anderson, David  
APPLICANT: Ballinger, Robert  
APPLICANT: Gerlach, Valerie  
APPLICANT: Spytek, Kimberly  
APPLICANT: Ratelli, Luca  
APPLICANT: Kekuda, Ramesh  
APPLICANT: Guo, Xiaojia  
APPLICANT: Zerhusen, Bryan  
APPLICANT: Andrew, David  
APPLICANT: Mezes, Peter  
APPLICANT: Patturajan, Meera  
APPLICANT: Burgess, Cahterine  
APPLICANT: Eisen, Andrew  
APPLICANT: Wolenc, Adam  
APPLICANT: Baumgartner, Jason  
APPLICANT: Shinkets, Richard  
APPLICANT: Gusev, Vladimir  
APPLICANT: Vernet, Corine  
APPLICANT: Taupier Jr., Raymond  
APPLICANT: Pena, Carol  
APPLICANT: Shenoy, Suresh  
APPLICANT: Li, Li  
APPLICANT: Casman, Stacie  
APPLICANT: Boldog, Ference  
TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoded Thereby  
FILE REFERENCE: 21402-251  
CURRENT APPLICATION NUMBER: US/10/055,877  
CURRENT FILING DATE: 2002-01-22  
PRIOR APPLICATION NUMBER: 60/262,892  
PRIOR FILING DATE: 2001-01-19  
PRIOR APPLICATION NUMBER: 60/263,598  
PRIOR FILING DATE: 2001-01-23  
PRIOR APPLICATION NUMBER: 60/263,799  
PRIOR FILING DATE: 2001-01-24  
PRIOR APPLICATION NUMBER: 60/264,117  
PRIOR FILING DATE: 2001-01-25  
PRIOR APPLICATION NUMBER: 60/264,139  
PRIOR FILING DATE: 2001-01-25  
PRIOR APPLICATION NUMBER: 60/264,478  
PRIOR FILING DATE: 2001-01-26

GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: March 22, 2006, 11:25:51 ; Search time 35.6667 Seconds  
(without alignments)  
1592.473 Million cell updates/sec

Title: US-10-612-668-21

Perfect score: 3620

Sequence: 1 MQPFGRLVNTFSGVTNLFNSN.....GAKELGRKVVDCCTDPDGRP 687

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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- 2: /cgm2\_6/ptodata/1/iaa/6\_COMB.pep.\*
- 3: /cgm2\_6/ptodata/1/iaa/H\_COMB.pep.\*
- 4: /cgm2\_6/ptodata/1/iaa/PCUTUS\_COMB.pep.\*
- 5: /cgm2\_6/ptodata/1/iaa/RE\_COMB.pep.\*
- 6: /cgm2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3620	100.0	687	1 US-08-555-568B-21	Sequence 21, Appl
2	3620	100.0	687	2 US-09-519-223-21	Sequence 21, Appl
3	3620	100.0	687	2 US-09-927-180-21	Sequence 21, Appl
4	3606.5	99.6	688	1 US-08-555-568B-23	Sequence 23, Appl
5	3606.5	99.6	688	2 US-09-519-223-23	Sequence 23, Appl
6	3606.5	99.6	688	2 US-09-927-180-23	Sequence 23, Appl
7	3566.5	98.5	819	2 US-09-949-016-10948	Sequence 10948, A
8	3302.5	91.2	752	1 US-08-281-193-2	Sequence 2, Appli
9	3302.5	91.2	752	1 US-08-422-106-2	Sequence 2, Appli
10	3302.5	91.2	752	1 US-08-735-716-2	Sequence 2, Appli
11	3302.5	91.2	752	1 US-08-555-568B-2	Sequence 2, Appli
12	3302.5	91.2	752	2 US-09-519-223-2	Sequence 2, Appli
13	3302.5	91.2	752	2 US-09-927-180-2	Sequence 2, Appli
14	3302.5	91.2	752	4 PCT-US95-08069-2	Sequence 2, Appli
15	2084	57.6	394	1 US-08-555-568B-17	Sequence 17, Appl
16	2084	57.6	394	2 US-09-519-223-17	Sequence 17, Appl
17	2084	57.6	394	2 US-09-927-180-17	Sequence 17, Appl
18	1531	42.3	292	1 US-08-555-568B-19	Sequence 19, Appl
19	1531	42.3	292	2 US-09-519-223-19	Sequence 19, Appl
20	1531	42.3	292	2 US-09-927-180-19	Sequence 19, Appl
21	1163.5	32.1	896	2 US-09-270-767-46130	Sequence 46130, A
22	902.5	24.9	545	2 US-09-270-767-61684	Sequence 61684, A
23	371	10.2	143	2 US-09-270-767-33298	Sequence 33298, A
24	338	9.3	843	1 US-09-172-977-3	Sequence 3, Appli
25	338	9.3	843	2 US-09-404-108-3	Sequence 3, Appli
26	332	9.2	1839	1 US-09-172-977-4	Sequence 4, Appli
27	332	9.2	1839	2 US-09-404-108-4	Sequence 4, Appli

28	332	9.2	2753	2	US-09-949-016-7659	Sequence 7659, Ap
29	332	9.2	2753	2	US-09-949-016-7660	Sequence 7660, Ap
30	332	9.2	3924	2	US-09-538-092-1246	Sequence 1246, Ap
31	305.5	8.4	1745	1	US-09-031-485-33	Sequence 33, Appl
32	305.5	8.4	1745	1	US-08-847-429A-33	Sequence 33, Appl
33	305.5	8.4	1745	2	US-09-065-474-33	Sequence 33, Appl
34	305.5	8.4	1745	2	US-09-557-034-33	Sequence 33, Appl
35	302	8.3	786	2	US-09-509-802-2	Sequence 2, Appli
36	302	8.3	787	2	US-09-188-930-334	Sequence 334, App
37	302	8.3	787	2	US-09-312-283C-334	Sequence 334, App
38	300.5	8.3	1724	2	US-09-964-899-43	Sequence 43, Appl
39	296	8.2	1088	2	US-09-082-059-2	Sequence 2, Appli
40	296	8.2	3913	2	US-09-949-016-10933	Sequence 10933, A
41	296	8.2	4377	2	US-09-949-016-6978	Sequence 6978, Ap
42	294	8.1	1719	2	US-09-949-016-6966	Sequence 6966, Ap
43	294	8.1	1856	2	US-09-949-016-6964	Sequence 6964, Ap
44	294	8.1	1880	2	US-09-949-016-5876	Sequence 5876, Ap
45	294	8.1	1881	2	US-09-949-016-6965	Sequence 6965, Ap

ALIGNMENTS

RESULT 1  
US-08-555-568B-21  
; Sequence 21, Application US/085555568B  
; Patent No. 5976854  
; GENERAL INFORMATION:  
; APPLICANT: Jones, Simon  
; APPLICANT: Tang, Jim  
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B  
; NUMBER OF SEQUENCES: 25  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: Genetics Institute, Inc.  
; STREET: 87 CambridgePark Drive  
; CITY: Cambridge  
; STATE: Massachusetts  
; COUNTRY: U.S.A.  
; ZIP: 02140  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/555,568B  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Brown, Scott A.  
; REGISTRATION NUMBER: 32,724  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 498-8224  
; TELEFAX: (617) 876-5851  
; INFORMATION FOR SEQ ID NO: 21:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 687 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-555-568B-21

Query Match	100.0%;	Score 3620;	DB 1;	Length 687;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 687;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MQPFGRLVNTFSGVTNLFNSNPFVKVAVADYTSRDRVREGQILILFQNTPNRTWDCVLV	60	
Db	1	MQPFGRLVNTFSGVTNLFNSNPFVKVAVADYTSRDRVREGQILILFQNTPNRTWDCVLV	60	
QY	61	NPNRSQSGRLFOLEADALVNPHQYSSQLLPFYESSPQVLHTEVQLHLDLRNHPSW	120	
Db	61	NPNRSQSGRLFOLEADALVNPHQYSSQLLPFYESSPQVLHTEVQLHLDLRNHPSW	120	

Qy	121	SV	AHLAVELGIRECFHHSRIISCANCAENEGCTPLHLACRKGDEILVELVOYCHTQMD	180
Db	121	SV	AHLAVELGIRECFHHSRIISCANCAENEGCTPLHLACRKGDEILVELVOYCHTQMD	180
Qy	181	VT	DYKGETVFHYAVOGDINSQVLILGRNAVAGLQVNNQGLTPLHLACOLGQEWVRVLL	240
Db	181	VT	DYKGETVFHYAVOGDINSQVLILGRNAVAGLQVNNQGLTPLHLACOLGQEWVRVLL	240
Qy	241	LC	NARCNIMGPNGYPIHSAKFSQKGCABMIISMDSSQIHSKDPXYGASPLHWAKNAEMA	300
Db	241	LC	NARCNIMGPNGYPIHSAKFSQKGCABMIISMDSSQIHSKDPXYGASPLHWAKNAEMA	300
Qy	301	RM	LLKRCGNVNSTSSAGNTALHVGVMRNFDCAIVLLTHGANADARGEHNTPLHLAMSK	360
Db	301	RM	LLKRCGNVNSTSSAGNTALHVGVMRNFDCAIVLLTHGANADARGEHNTPLHLAMSK	360
Qy	361	DN	VEMIKALIIVFGAEVDTPNDFGETPTFLASKIGKLQDLMHISRARKPAFILGSMRDEKR	420
Db	361	DN	VEMIKALIIVFGAEVDTPNDFGETPTFLASKIGKLQDLMHISRARKPAFILGSMRDEKR	420
Qy	421	TH	DHLLCLDGGGVKGLIIQLLIAIEKASGVATKDLFDWVAGTSTGGIILALILHSKSNA	480
Db	421	TH	DHLLCLDGGGVKGLIIQLLIAIEKASGVATKDLFDWVAGTSTGGIILALILHSKSNA	480
Qy	481	YMR	GMYFRMKDEVFRGSRPYESGPLEEFUKREFGHEHTKMTDVRKPKVMLTGTLSDRQPAE	540
Db	481	YMR	GMYFRMKDEVFRGSRPYESGPLEEFUKREFGHEHTKMTDVRKPKVMLTGTLSDRQPAE	540
Qy	541	LHL	FRNYDAPETVREPRFNQVNLRPAPQPSDQLVWRAARSSGAAPTVPFRNGRFLDGLG	600
Db	541	LHL	FRNYDAPETVREPRFNQVNLRPAPQPSDQLVWRAARSSGAAPTVPFRNGRFLDGLG	600
Qy	601	LANN	PTLDAMTEIHEYNDLIRKGOANKVKKLSIIVVSLGTGRSPQVPVTCVDVFRPSNPW	660
Db	601	LANN	PTLDAMTEIHEYNDLIRKGOANKVKKLSIIVVSLGTGRSPQVPVTCVDVFRPSNPW	660
Qy	661	ELAK	TVFGAKELGRKMWDCCTDPDGRP	687
Db	661	ELAK	TVFGAKELGRKMWDCCTDPDGRP	687

## RESULT 2

US-09-519-223-21  
; Sequence 21, Application US/09519223  
; Patent No. 6274140  
; GENERAL INFORMATION:  
; APPLICANT: Jones, Simon  
; APPLICANT: Tang, Jim  
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B  
; NUMBER OF SEQUENCES: 25  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genetics Institute, Inc.  
; STREET: 87 CambridgePark Drive  
; CITY: Cambridge  
; STATE: Massachusetts  
; COUNTRY: U.S.A.  
; ZIP: 02140  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/519,223  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/555,568  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Brown, Scott A.  
; REGISTRATION NUMBER: 32,724

GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: March 22, 2006, 12:00:11 ; Search time 120.175 Seconds  
(without alignments)  
2392.073 Million cell updates/sec

Title: US-10-612-668-23

Perfect score: 3625

Sequence: 1 MQFGRLVNTFSGVTNLFNSN.....GAKELGRMVDCCTDPDRP 688

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA Main:  
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4: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep.\*  
5: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*  
6: /cgn2\_6/ptodata/1/pubpaa/US11\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3625	100.0	688	3	US-09-927-180-23
2	3625	100.0	688	5	US-10-612-668-23
3	3606.5	99.5	687	3	US-09-927-180-21
4	3606.5	99.5	687	5	US-10-612-668-21
5	3315	91.4	752	3	US-09-927-180-2
6	3315	91.4	752	5	US-10-612-668-2
7	2728.5	75.3	667	4	US-10-108-260A-3778
8	2084	57.5	394	3	US-09-927-180-17
9	2084	57.5	394	5	US-10-612-668-17
10	1531	42.2	292	3	US-09-927-180-19
11	1531	42.2	292	5	US-10-612-668-19
12	1165	32.1	877	6	US-11-097-143-14664
13	651	18.0	1071	4	US-10-369-493-6865
14	627	17.3	1023	4	US-10-369-493-6689
15	627	17.3	1023	4	US-10-369-493-6690
16	326	9.0	468	4	US-10-369-493-4998
17	324	8.9	1330	4	US-10-108-260A-3237
18	319.5	8.8	1549	6	US-11-097-143-1776
19	319.5	8.8	1549	6	US-11-097-143-29028
20	302.5	8.3	2443	6	US-11-097-143-8355
21	301.5	8.3	786	4	US-10-164-080-2
22	301.5	8.3	786	4	US-10-299-327-2
23	301.5	8.3	786	4	US-10-128-174-13
24	301.5	8.3	786	4	US-10-128-174-31
25	301.5	8.3	786	4	US-10-128-174-32
26	301.5	8.3	786	4	US-10-128-174-33
27	301.5	8.3	787	3	US-09-866-050A-334

28	301.5	8.3	1724	3	US-09-964-899-43	Sequence 43, Appl
29	301.5	8.3	1724	5	US-10-975-523-43	Sequence 43, Appl
30	301	8.3	347	4	US-10-128-174-30	Sequence 30, Appl
31	296	8.2	1094	5	US-10-479-764-22	Sequence 22, Appl
32	296	8.2	1097	5	US-10-450-763-52300	Sequence 52300, A
33	296	8.2	3913	4	US-10-334-143-45	Sequence 45, Appl
34	296	8.2	4274	5	US-10-450-763-31331	Sequence 31331, A
35	296	8.2	4377	5	US-10-756-149-4917	Sequence 4917, Ap
36	296	8.2	4386	5	US-10-450-763-37734	Sequence 37734, A
37	296	8.2	4397	5	US-10-450-763-52303	Sequence 52303, A
38	293.5	8.1	1762	4	US-10-205-194-117	Sequence 117, App
39	286.5	7.9	720	4	US-10-433-794-20	Sequence 20, Appl
40	286.5	7.9	765	4	US-10-128-174-3	Sequence 3, Appl
41	286.5	7.9	765	4	US-10-128-174-34	Sequence 34, Appl
42	286.5	7.9	765	4	US-10-128-174-35	Sequence 35, Appl
43	286.5	7.9	765	4	US-10-128-174-36	Sequence 36, Appl
44	286.5	7.9	765	4	US-10-128-174-37	Sequence 37, Appl
45	286.5	7.9	765	4	US-10-128-174-38	Sequence 38, Appl

ALIGNMENTS

RESULT 1

US-09-927-180-23  
; Sequence 23, Application US/09927180  
; Patent No. US20020106364A1  
; GENERAL INFORMATION:  
; APPLICANT: Jones, Simon  
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B  
; NUMBER OF SEQUENCES: 25  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genetics Institute, Inc.  
; STREET: 87 Cambridgepark Drive  
; CITY: Cambridge  
; STATE: Massachusetts  
; COUNTRY: U.S.A.  
; ZIP: 02140  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/927,180  
; FILING DATE: 09-Aug-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/519,223  
; FILING DATE: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Brown, Scott A.  
; REGISTRATION NUMBER: 32,724  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 498-8224  
; TELEFAX: (617) 876-5851  
; INFORMATION FOR SEQ ID NO: 23:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 688 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: Protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 23:  
US-09-927-180-23

Query Match 100.0%; Score 3625; DB 3; Length 688;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 688; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQFGRLVNTFSGVTNLFNSNPRVKEVAVADYTSRVRREGQLILFQNTPNRTDCVLV 60  
|||||  
DB 1 MQFGRLVNTFSGVTNLFNSNPRVKEVAVADYTSRVRREGQLILFQNTPNRTDCVLV 60  
|||||

61 NPNSSQSGFRLFOLELEADALVNFHOYSQOLLFFYESSPOVLHTEVQLHQLTDLIRNHPW 120  
61 NPNSSQSGFRLFOLELEADALVNFHOYSQOLLFFYESSPOVLHTEVQLHQLTDLIRNHPW 120  
121 SVAHLAVELGIRCFHHSRIISCANCAENEEGCTPLHLACRKGDEGILVELVOYCHTQMD 180  
121 SVAHLAVELGIRCFHHSRIISCANCAENEEGCTPLHLACRKGDEGILVELVOYCHTQMD 180  
181 VTDYKGETVFHYAVQGDNSQVLQGLGRNAVAGLNQVNNQGLTPLHLACOLGKQEMVRVLL 240  
181 VTDYKGETVFHYAVQGDNSQVLQGLGRNAVAGLNQVNNQGLTPLHLACOLGKQEMVRVLL 240  
241 LCNARCINMGPNPGYPIHSAMKFSQKCAEMIIISMDSSQIHSKDPYRGASPLHWAKNAEMA 300  
241 LCNARCINMGPNPGYPIHSAMKFSQKCAEMIIISMDSSQIHSKDPYRGASPLHWAKNAEMA 300  
301 RMLLKRGCVNSTSSAGNTALHVGVMNRNRPDCAIVLLTHGANADARGEHNTPLHLAMSK 360  
301 RMLLKRGCVNSTSSAGNTALHVGVMNRNRPDCAIVLLTHGANADARGEHNTPLHLAMSK 360  
361 DNVEMIKALIVFGAEVDTNDFGETPTFLASKIGROLDLMIHSRARKPAFILGSMRDEK 420  
361 DNVEMIKALIVFGAEVDTNDFGETPTFLASKIGROLDLMIHSRARKPAFILGSMRDEK 420  
421 RTHDHLCLDGGGVKGLIIIIQLLIAIEKASGVATKDLFDWVAGTSTGGILALAILHLSKSM 480  
421 RTHDHLCLDGGGVKGLIIIIQLLIAIEKASGVATKDLFDWVAGTSTGGILALAILHLSKSM 480  
481 AYMRGMVFRMKDVEFRGSRPYESGLEFLKREFGEHTKMTDVRKPKVMTGTLSDRQPA 540  
481 AYMRGMVFRMKDVEFRGSRPYESGLEFLKREFGEHTKMTDVRKPKVMTGTLSDRQPA 540  
541 ELHLFRNYDAPETVREPRFNQNVNLRPPAQSOLVWRAARSSGAAPTFRNGRFLDGG 600  
541 ELHLFRNYDAPETVREPRFNQNVNLRPPAQSOLVWRAARSSGAAPTFRNGRFLDGG 600  
601 LLANNPTLDAMTEIHEYNOQLIRKQANKVKLSIVVSLGTGRSPQVPVTCVDVFRPSNP 660  
601 LLANNPTLDAMTEIHEYNOQLIRKQANKVKLSIVVSLGTGRSPQVPVTCVDVFRPSNP 660  
661 WELAKTVFGAKELGKMVVDCCCTDPDGRP 688  
661 WELAKTVFGAKELGKMVVDCCCTDPDGRP 688

## RESULT 2

US-10-612-668-23  
Sequence 23, Application US/10612668  
Publication No. US20050196852A1  
GENERAL INFORMATION:  
APPLICANT: Jones, Simon  
Tang, Jim  
TITLE OF INVENTION: Calcium Independent Phospholipase A2/B  
NUMBER OF SEQUENCES: 25  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genetics Institute, Inc.  
STREET: 87 CambridgePark Drive  
CITY: Cambridge  
STATE: Massachusetts  
COUNTRY: U.S.A.  
ZIP: 02140  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25 (BPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/612,668  
FILING DATE: 01-Jul-2003  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/927,180

FILING DATE: 09-Aug-2001  
APPLICATION NUMBER: 09/519,223  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Brown, Scott A.  
REGISTRATION NUMBER: 32,724  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 498-8224  
TELEFAX: (617) 876-5851  
INFORMATION FOR SEQ ID NO: 23:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 688 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 23:  
US-10-612-668-23  
Query Match 100.0%; Score 3625; DB 5; Length 688;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 688; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MOFFRLVNTFSGVTNLFSPNPRVKEVAVADYTSSDRVREGQLILFQNTPNRTWDCVLV 60  
DB 1 MOFFRLVNTFSGVTNLFSPNPRVKEVAVADYTSSDRVREGQLILFQNTPNRTWDCVLV 60  
QY 61 NPNSSQSGFRLFOLELEADALVNFHOYSQOLLFFYESSPOVLHTEVQLHQLTDLIRNHPW 120  
DB 61 NPNSSQSGFRLFOLELEADALVNFHOYSQOLLFFYESSPOVLHTEVQLHQLTDLIRNHPW 120  
QY 121 SVAHLAVELGIRCFHHSRIISCANCAENEEGCTPLHLACRKGDEGILVELVOYCHTQMD 180  
DB 121 SVAHLAVELGIRCFHHSRIISCANCAENEEGCTPLHLACRKGDEGILVELVOYCHTQMD 180  
QY 181 VTDYKGETVFHYAVQGDNSQVLQGLGRNAVAGLNQVNNQGLTPLHLACOLGKQEMVRVLL 240  
DB 181 VTDYKGETVFHYAVQGDNSQVLQGLGRNAVAGLNQVNNQGLTPLHLACOLGKQEMVRVLL 240  
QY 241 LCNARCINMGPNPGYPIHSAMKFSQKCAEMIIISMDSSQIHSKDPYRGASPLHWAKNAEMA 300  
DB 241 LCNARCINMGPNPGYPIHSAMKFSQKCAEMIIISMDSSQIHSKDPYRGASPLHWAKNAEMA 300  
QY 301 RMLLKRGCVNSTSSAGNTALHVGVMNRNRPDCAIVLLTHGANADARGEHNTPLHLAMSK 360  
DB 301 RMLLKRGCVNSTSSAGNTALHVGVMNRNRPDCAIVLLTHGANADARGEHNTPLHLAMSK 360  
QY 361 DNVEMIKALIVFGAEVDTNDFGETPTFLASKIGROLDLMIHSRARKPAFILGSMRDEK 420  
DB 361 DNVEMIKALIVFGAEVDTNDFGETPTFLASKIGROLDLMIHSRARKPAFILGSMRDEK 420  
QY 421 RTHDHLCLDGGGVKGLIIIIQLLIAIEKASGVATKDLFDWVAGTSTGGILALAILHLSKSM 480  
DB 421 RTHDHLCLDGGGVKGLIIIIQLLIAIEKASGVATKDLFDWVAGTSTGGILALAILHLSKSM 480  
QY 481 AYMRGMVFRMKDVEFRGSRPYESGLEFLKREFGEHTKMTDVRKPKVMTGTLSDRQPA 540  
DB 481 AYMRGMVFRMKDVEFRGSRPYESGLEFLKREFGEHTKMTDVRKPKVMTGTLSDRQPA 540  
QY 541 ELHLFRNYDAPETVREPRFNQNVNLRPPAQSOLVWRAARSSGAAPTFRNGRFLDGG 600  
DB 541 ELHLFRNYDAPETVREPRFNQNVNLRPPAQSOLVWRAARSSGAAPTFRNGRFLDGG 600  
QY 601 LLANNPTLDAMTEIHEYNOQLIRKQANKVKLSIVVSLGTGRSPQVPVTCVDVFRPSNP 660  
DB 601 LLANNPTLDAMTEIHEYNOQLIRKQANKVKLSIVVSLGTGRSPQVPVTCVDVFRPSNP 660  
QY 661 WELAKTVFGAKELGKMVVDCCCTDPDGRP 688  
DB 661 WELAKTVFGAKELGKMVVDCCCTDPDGRP 688

## RESULT 3

US-09-927-180-21

GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: March 22, 2006, 12:01:45 ; Search time 15.0218 Seconds  
(without alignments)  
1310.928 Million cell updates/sec

Title: US-10-612-668-23

Perfect score: 3625

Sequence: 1 MQFGRLVNTSGVNLFSN.....GAKELGVNVDCCTDPDGRP 688

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 169630 seqs, 28622899 residues

Total number of hits satisfying chosen parameters: 169630

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA New:

- 1: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB\_PEP.\*
- 2: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB\_PEP.\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB\_PEP.\*
- 4: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB\_PEP.\*
- 5: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB\_PEP.\*
- 6: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB\_PEP.\*
- 7: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB\_PEP.\*
- 8: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB\_PEP.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	310	8.6	1159	6	US-10-055-877-139
2	296	8.2	1765	6	US-10-055-877-140
3	296	8.2	1940	6	US-10-055-877-141
4	296	8.2	4384	6	US-10-821-234-1120
5	281	7.8	784	7	US-11-072-175-153
6	271.5	7.5	1059	6	US-10-055-877-138
7	263.5	7.3	1431	6	US-10-501-035-220
8	252	7.0	795	7	US-11-072-512-2378
9	249	6.9	791	6	US-10-055-877-137
10	244	6.7	237	7	US-11-096-568A-28113
11	244	6.7	247	7	US-11-096-568A-28112
12	238	6.6	831	7	US-11-096-568A-1542
13	236	6.5	993	6	US-10-055-877-6
14	233	6.4	784	7	US-11-096-568A-22417
15	229.5	6.3	240	7	US-11-096-568A-22416
16	229.5	6.3	244	7	US-11-096-568A-22416
17	229.5	6.3	645	7	US-11-072-512-2588
18	227	6.3	505	7	US-11-072-512-2553
19	223	6.2	219	7	US-11-096-568A-28114
20	214.5	5.9	241	7	US-11-096-568A-9945
21	214.5	5.9	245	7	US-11-096-568A-9944
22	214.5	5.9	280	7	US-11-096-568A-9943
23	211.5	5.8	657	7	US-11-072-512-2529
24	209.5	5.8	1719	7	US-11-234-786-378
25	209.5	5.8	2471	7	US-11-050-346-68

Sequence 379, App  
Sequence 380, App  
Sequence 67, Appl  
Sequence 1544, Ap  
Sequence 8, Appl  
Sequence 3088, Ap  
Sequence 3091, Ap  
Sequence 2, Appl  
Sequence 376, App  
Sequence 32354, A  
Sequence 32353, A  
Sequence 2675, Ap  
Sequence 532, App  
Sequence 16313, A  
Sequence 16312, A  
Sequence 11369, A  
Sequence 11368, A  
Sequence 11367, A  
Sequence 93, Appl  
Sequence 975, App

#### ALIGNMENTS

RESULT 1  
US-10-055-877-139  
; Sequence 139, Application US/10055877  
; Publication No. US20050288241A1  
; GENERAL INFORMATION:

; APPLICANT: Decristofaro, Marc  
; APPLICANT: Padigaru, Muralidhara  
; APPLICANT: Miller, Charles  
; APPLICANT: Tchernev, Velizar  
; APPLICANT: Zhong, Mei  
; APPLICANT: Anderson, David  
; APPLICANT: Ballinger, Robert  
; APPLICANT: Gerlach, Valerie  
; APPLICANT: Spytek, Kimberly  
; APPLICANT: Ratelli, Luca  
; APPLICANT: Kekuda, Ramesh  
; APPLICANT: Guo, Xiaojia  
; APPLICANT: Zerhusen, Bryan  
; APPLICANT: Mezes, Peter  
; APPLICANT: Patturajan, Meera  
; APPLICANT: Burgess, Catherine  
; APPLICANT: Eisen, Andrew  
; APPLICANT: Wolenc, Adam  
; APPLICANT: Baumgartner, Jason  
; APPLICANT: Shimkets, Richard  
; APPLICANT: Gusev, Vladimir  
; APPLICANT: Vernet, Corine  
; APPLICANT: Taupier Jr., Raymond  
; APPLICANT: Pena, Carol  
; APPLICANT: Shenoy, Suresh  
; APPLICANT: Li, Li  
; APPLICANT: Casman, Stacie  
; APPLICANT: Baldog, Ference  
; TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoded Thereby  
; FILE REFERENCE: 21402-251  
; CURRENT FILING DATE: 2002-01-22  
; PRIOR APPLICATION NUMBER: 60/262,892  
; PRIOR FILING DATE: 2001-01-19  
; PRIOR APPLICATION NUMBER: 60/263,598  
; PRIOR FILING DATE: 2001-01-23  
; PRIOR APPLICATION NUMBER: 60/263,799  
; PRIOR FILING DATE: 2001-01-24  
; PRIOR APPLICATION NUMBER: 60/264,117  
; PRIOR FILING DATE: 2001-01-25  
; PRIOR APPLICATION NUMBER: 60/264,139  
; PRIOR FILING DATE: 2001-01-25



Result No.	Score	Query		Length	DB	ID	Description
		Match	%				
1	3625	100.0	688	1	US-08-555-568B-23		Sequence 23, Appl
2	3625	100.0	688	2	US-09-519-223-23		Sequence 23, Appl
3	3625	100.0	688	2	US-09-927-180-23		Sequence 23, Appl
4	3606.5	99.5	687	1	US-08-555-568B-21		Sequence 21, Appl
5	3606.5	99.5	687	2	US-09-519-223-21		Sequence 21, Appl
6	3606.5	99.5	687	2	US-09-927-180-21		Sequence 21, Appl
7	3372	98.5	819	2	US-09-949-016-10948		Sequence 10948, A
8	3315	91.4	752	1	US-08-281-193-2		Sequence 2, Appl
9	3315	91.4	752	1	US-08-422-106-2		Sequence 2, Appl
10	3315	91.4	752	1	US-08-735-716-2		Sequence 2, Appl
11	3315	91.4	752	1	US-08-555-568B-2		Sequence 2, Appl
12	3315	91.4	752	2	US-09-519-223-2		Sequence 2, Appl
13	3315	91.4	752	2	US-09-927-180-2		Sequence 2, Appl
14	3315	91.4	752	4	PCR-US95-08069-2		Sequence 2, Appl
15	2084	57.5	394	1	US-08-555-568B-17		Sequence 17, Appl
16	2084	57.5	394	2	US-09-519-223-17		Sequence 17, Appl
17	2084	57.5	394	2	US-09-927-180-17		Sequence 17, Appl
18	1531	42.2	292	1	US-08-555-568B-19		Sequence 19, Appl
19	1531	42.2	292	2	US-09-519-223-19		Sequence 19, Appl
20	1531	42.2	292	2	US-09-927-180-19		Sequence 19, Appl
21	1165	32.1	896	2	US-09-270-767-46130		Sequence 46130, A
22	904	24.9	545	2	US-09-270-767-61684		Sequence 61684, A
23	371	10.2	143	2	US-09-270-767-33298		Sequence 33298, A
24	338	9.3	843	1	US-09-170-977-3		Sequence 3, Appl
25	338	9.3	843	2	US-09-404-108-3		Sequence 3, Appl
26	332	9.2	1839	1	US-09-172-977-4		Sequence 4, Appl
27	332	9.2	1839	2	US-09-404-108-4		Sequence 4, Appl

121 SVAHLAVELGIRECFHHSRIISCANCAENEEGCTPLHLACRKGDEGLVELVOYCHTOMD 180  
121 SVAHLAVELGIRECFHHSRIISCANCAENEEGCTPLHLACRKGDEGLVELVOYCHTOMD 180  
181 VTDYKGETVPHYAVQGDNSOVQLLGRNAVAGLNVNNOGLTPLHLACQLGKQEMVRVLL 240  
181 VTDYKGETVPHYAVQGDNSOVQLLGRNAVAGLNVNNOGLTPLHLACQLGKQEMVRVLL 240  
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421 RTHDHLCLDGGVKGILIIQLLIAIEKASGVATKDLFDWVAGTSTGGILALAILHLSKSM 480  
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601 LLANNPTLDAMTEIHEYNOQLIRKQANKVKLSIVVSLGTGRSPQVPTCVDFVRPSNP 660  
661 WELAKTVFGAKELGKMWVDCCTDPDGRP 688  
661 WELAKTVFGAKELGKMWVDCCTDPDGRP 688

## RESULT 2

US-09-519-223-23  
Sequence 23, Application US/09519223  
Patent No. 6274140  
GENERAL INFORMATION:  
APPLICANT: Jones, Simon  
APPLICANT: Tang, Jim  
TITLE OF INVENTION: Calcium Independent Phospholipase A2/B  
NUMBER OF SEQUENCES: 25  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genetics Institute, Inc.  
STREET: 87 CambridgePark Drive  
CITY: Cambridge  
STATE: Massachusetts  
COUNTRY: U.S.A.  
ZIP: 02140  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/519,223  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/555,568  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Brown, Scott A.  
REGISTRATION NUMBER: 32,724

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 498-8224  
TELEFAX: (617) 876-5851  
INFORMATION FOR SEQ ID NO: 23:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 688 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-519-223-23

Query Match 100.0%; Score 3625; DB 2; Length 688;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 688; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MOFFGRLVNTFSGVNTLFSNPRVKEVAVADYSSDRVREEGQLIIFQNTPNRTWDCVLV 60  
QY 61 NPNRSQSGFRLFQLEADALVNFHYSSQLLPFYESSQVLTHTVLOHLDLIRNHPWS 120  
DB 61 NPNRSQSGFRLFQLEADALVNFHYSSQLLPFYESSQVLTHTVLOHLDLIRNHPWS 120  
QY 121 SVAHLAVELGIRECFHHSRIISCANCAENEEGCTPLHLACRKGDEGLVELVOYCHTOMD 180  
DB 121 SVAHLAVELGIRECFHHSRIISCANCAENEEGCTPLHLACRKGDEGLVELVOYCHTOMD 180  
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DB 181 VTDYKGETVPHYAVQGDNSOVQLLGRNAVAGLNVNNOGLTPLHLACQLGKQEMVRVLL 240  
QY 241 LCNARCNIMGPNYPIHSAKFSGKCAEMIISDSSQIHSKDPYRGASPLHWAKNAEMA 300  
DB 241 LCNARCNIMGPNYPIHSAKFSGKCAEMIISDSSQIHSKDPYRGASPLHWAKNAEMA 300  
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QY 541 ELHLFRNYDAPETVREPRFNQNVNLRPPAQPSDQVWRAARSSGAAPTFRPNRFLDGG 600  
DB 541 ELHLFRNYDAPETVREPRFNQNVNLRPPAQPSDQVWRAARSSGAAPTFRPNRFLDGG 600  
QY 601 LLANNPTLDAMTEIHEYNOQLIRKQANKVKLSIVVSLGTGRSPQVPTCVDFVRPSNP 660  
DB 601 LLANNPTLDAMTEIHEYNOQLIRKQANKVKLSIVVSLGTGRSPQVPTCVDFVRPSNP 660  
QY 661 WELAKTVFGAKELGKMWVDCCTDPDGRP 688  
DB 661 WELAKTVFGAKELGKMWVDCCTDPDGRP 688

## RESULT 3

US-09-927-180-23  
Sequence 23, Application US/09927180  
Patent No. 6645736  
GENERAL INFORMATION:  
APPLICANT: Jones, Simon  
APPLICANT: Tang, Jim  
TITLE OF INVENTION: Calcium Independent Phospholipase A2/B  
NUMBER OF SEQUENCES: 25